

FIG. 1

ATGGCGCCGCGCCGCGCCGCGCGCTGCTGCCCCGTGCTGCTGCTCCTGGCCGCGCCGCGCCGCGCCCTGCCGGCGATGGGGCTGCG
 AGCGGCGCGCTGGGAGCCGCGGTACCCGGCGGGACCCGCGCCCTTCGCCCTCCGGCCCGGCTGTACCTACGCGGTGGGCG
 CCGCTTGACAGCCCCGCGCCGCGCGGGAGCTGCTGGACGTGGGCGCGCATGGGCGGCTGGCAGGACGTCGGCGCGTCTCG
 GCGCGCGGGCGCCCGCTGCCGCTGCAAGTCCGCTTGCTGGCCCGCAGTGCCCCGACGGCGCTGAGCCGCGCGCTGCCGGC
 GCGCACGCACCTTCCCGGCTGCCGAGCCCGTGCCCGGCTCTGCGGAACCGGTGCCCGGCTCTGCGGGGCGCTCTGCTTCC
 CCGTCCCCGGCGGCTGCCGCGCGCGCAGCATTGCGCGCTCGCAGCTCCGACCACCTTACCCGCTGCCGCTGCCCGCGC
 CGCCCCAGGCCCCGCTGTCCCGGCGCTCCCATCTGCTGCCCGCGGGCGGCTCGGTCCGCTGCGTCTGCTGTGCGCCCT
 GCGGCGCGCGGCTGCCGCGCTCCGGGTGGGACTGGCGCTGGAGGCCGCCACCCCGGGACGCCCTCCGCTGCCCATCCC
 CATCGCCGCCCCCTGCCGCGCAACTTGCCCCGAAGCCCGGGCGGGGCGCGCGACGGGCCCGGCGGGGCGACGCGCGCAGA
 GGGAGCCTGAAGTTTCCGATGCCCAACTACAGGTGGCGTTGTTTGAGAACGAACCGGCGGGCACCCCTCATCTCCAGCT
 GCACCGCACTACACCATCGAGGGCGAGGAGGAGCGCGTGAGCTATTACATGGAGGGGCTGTTCGACGAGCGCTCCCGGG
 GCTACTTCCGAATCGACTCTGCCACGGGCGCGGTGAGCACGGACAGCGTACTGGACCGCGAGACCAAGGAGACGCACGTC
 CTCAGGGTGAAAGCCGTGGACTACAGTACGCGCGCGCGCTCGGCCACACCTACATCACTGTCTTGCTCAAAGACACCAA
 CGACCACAGCCCGGCTTTCGAGCAGTCGGAGTACCGCGAGCGGTGCGGGAGAACCCTGGAGGTGGGCTACGAGGTGCTGA
 CCATCCGCGCCAGCGACCCGACTCGCCCATCAACGCCAACTTGCGTTACCCGCTGTTGGGGGGCGCGTGGGACGTCTTC
 CAGCTCAACGAGAGCTCTGGCGTGGTGAGCACACGGGCGGTGCTGGACCGGGAGGAGGCGGCCGAGTACCAGCTCCTGGT
 GGAGGCCAACGACCAGGGCGCAATCCGGGCGCGCTCAGTGCCACGGCCACCGTGTACATCGAGGTGGAGGACGAGAACG
 ACAACTACCCCACTTCAGCGAGCAGAACTACGTGGTCCAGGTGCCCGAGGACGTGGGGCTCAACACGGCTGTGCTGCGA
 GTGCAGGGCCACGGACCGGGACCGGGCCAGACGCGGCCATTCACTACAGCATCCTCAGCGGGAACGTGGCCGCGCAATT
 CTACCTGCACTCGCTGAGCGGGATCCTGGATGTGATCAACCCCTTGATTTTCGAGGATGTCCAGAAATACTCGCTGAGCA
 TTAAGGCCCAGGATGGGGGCGGCCCCCGCTCATCAATTCTTCAGGGGTGGTGTCTGTGCAGGTGCTGGATGTCAACGAC
 AACGAGCCTATCTTTGTGAGCAGCCCTTCCAGGCCACGGTGTGCGAGAATGTGCCCTGGGCTACCCCGTGGTGCACAT
 TCAGGCGGTGGACGCGGACTCTGGAGAGAACGCCCGGCTGCACTATCGCCTGGTGGACACGGCTCCACCTTTCTGGGGG
 GCGGCAGCGCTGGGCGCTAAGAATCTGCCCCACCCCTGACTTCCCTTCCAGATCCACAACAGCTCCGGTTGGATCACA
 GTGTGTGCCGAGCTGGACCGCGAGGAGGTGGAGCACTACAGCTTCGGGGTGGAGGCGGTGGACCACGGCTCGCCCCCAT
 GAGCTCCTCCACCAGCGTGTCCATCACGGTGCTGGACGTGAATGACAACGACCCGGTGTTCACGCAGCCACCTACGAGC
 TTCGTCTGAATGAGGATGCGGCGCGTGGGGAGCAGCGTGCTGACCTGCAGGCCCCGACCGTGACGCCAACAGTGTGATT
 ACCTACCAGCTCACAGGCGGCAACACCCGGAACCGCTTTGCACTCAGCAGCCAGAGAGGGGGCGGCTCATCACCCCTGGC
 GCTACCTCTGGACTACAAGCAGGAGCAGCAGTACGTGCTGGCGGTGACAGCATCCGACGGCACACGGTCCGACACTGCGC
 ATGTCTAATCAACGTCACTGATGCCAACACCCACAGGCGCTGCTTTTCAGAGCTCCATTACACAGTGAGTGTCAGTGAG
 GACAGGCGCTGTGGGCACTTCCATTGCTACCTCAGTGCCAACGATGAGGACACAGAGAGAATGCCCGCATCACCTACGT
 GATTCAGGACCCCGTGCCGCGAGTTCCGCATTGACCCCGACAGTGCCACCATGTACACCATGATGGAGCTGGACTATGAGA

| DATE | DESCRIPTION | AMOUNT | BALANCE |
|------|-------------|---------|-----------|
| 1870 | Jan 1 | | 100.00 |
| 1871 | Feb 1 | 50.00 | 150.00 |
| 1872 | Mar 1 | 25.00 | 175.00 |
| 1873 | Apr 1 | 75.00 | 250.00 |
| 1874 | May 1 | 100.00 | 350.00 |
| 1875 | Jun 1 | 150.00 | 500.00 |
| 1876 | Jul 1 | 200.00 | 700.00 |
| 1877 | Aug 1 | 250.00 | 950.00 |
| 1878 | Sep 1 | 300.00 | 1250.00 |
| 1879 | Oct 1 | 350.00 | 1600.00 |
| 1880 | Nov 1 | 400.00 | 2000.00 |
| 1881 | Dec 1 | 450.00 | 2450.00 |
| 1882 | Jan 1 | 500.00 | 2950.00 |
| 1883 | Feb 1 | 550.00 | 3500.00 |
| 1884 | Mar 1 | 600.00 | 4100.00 |
| 1885 | Apr 1 | 650.00 | 4750.00 |
| 1886 | May 1 | 700.00 | 5450.00 |
| 1887 | Jun 1 | 750.00 | 6200.00 |
| 1888 | Jul 1 | 800.00 | 7000.00 |
| 1889 | Aug 1 | 850.00 | 7850.00 |
| 1890 | Sep 1 | 900.00 | 8750.00 |
| 1891 | Oct 1 | 950.00 | 9700.00 |
| 1892 | Nov 1 | 1000.00 | 10700.00 |
| 1893 | Dec 1 | 1050.00 | 11750.00 |
| 1894 | Jan 1 | 1100.00 | 12850.00 |
| 1895 | Feb 1 | 1150.00 | 14000.00 |
| 1896 | Mar 1 | 1200.00 | 15200.00 |
| 1897 | Apr 1 | 1250.00 | 16450.00 |
| 1898 | May 1 | 1300.00 | 17750.00 |
| 1899 | Jun 1 | 1350.00 | 19100.00 |
| 1900 | Jul 1 | 1400.00 | 20500.00 |
| 1901 | Aug 1 | 1450.00 | 21950.00 |
| 1902 | Sep 1 | 1500.00 | 23450.00 |
| 1903 | Oct 1 | 1550.00 | 25000.00 |
| 1904 | Nov 1 | 1600.00 | 26600.00 |
| 1905 | Dec 1 | 1650.00 | 28250.00 |
| 1906 | Jan 1 | 1700.00 | 29950.00 |
| 1907 | Feb 1 | 1750.00 | 31700.00 |
| 1908 | Mar 1 | 1800.00 | 33500.00 |
| 1909 | Apr 1 | 1850.00 | 35350.00 |
| 1910 | May 1 | 1900.00 | 37250.00 |
| 1911 | Jun 1 | 1950.00 | 39200.00 |
| 1912 | Jul 1 | 2000.00 | 41200.00 |
| 1913 | Aug 1 | 2050.00 | 43250.00 |
| 1914 | Sep 1 | 2100.00 | 45350.00 |
| 1915 | Oct 1 | 2150.00 | 47500.00 |
| 1916 | Nov 1 | 2200.00 | 49700.00 |
| 1917 | Dec 1 | 2250.00 | 51950.00 |
| 1918 | Jan 1 | 2300.00 | 54250.00 |
| 1919 | Feb 1 | 2350.00 | 56600.00 |
| 1920 | Mar 1 | 2400.00 | 59000.00 |
| 1921 | Apr 1 | 2450.00 | 61450.00 |
| 1922 | May 1 | 2500.00 | 63950.00 |
| 1923 | Jun 1 | 2550.00 | 66500.00 |
| 1924 | Jul 1 | 2600.00 | 69100.00 |
| 1925 | Aug 1 | 2650.00 | 71750.00 |
| 1926 | Sep 1 | 2700.00 | 74450.00 |
| 1927 | Oct 1 | 2750.00 | 77200.00 |
| 1928 | Nov 1 | 2800.00 | 80000.00 |
| 1929 | Dec 1 | 2850.00 | 82850.00 |
| 1930 | Jan 1 | 2900.00 | 85750.00 |
| 1931 | Feb 1 | 2950.00 | 88700.00 |
| 1932 | Mar 1 | 3000.00 | 91700.00 |
| 1933 | Apr 1 | 3050.00 | 94750.00 |
| 1934 | May 1 | 3100.00 | 97850.00 |
| 1935 | Jun 1 | 3150.00 | 101000.00 |
| 1936 | Jul 1 | 3200.00 | 104200.00 |
| 1937 | Aug 1 | 3250.00 | 107450.00 |
| 1938 | Sep 1 | 3300.00 | 110750.00 |
| 1939 | Oct 1 | 3350.00 | 114100.00 |
| 1940 | Nov 1 | 3400.00 | 117500.00 |
| 1941 | Dec 1 | 3450.00 | 120950.00 |
| 1942 | Jan 1 | 3500.00 | 124450.00 |
| 1943 | Feb 1 | 3550.00 | 128000.00 |
| 1944 | Mar 1 | 3600.00 | 131600.00 |
| 1945 | Apr 1 | 3650.00 | 135250.00 |
| 1946 | May 1 | 3700.00 | 138950.00 |
| 1947 | | | |

ACGAGGTCGCTACACGCTGACCATCATGCGCCAGGACAAACGGCATCCCGCAGAAATCAGACACACCCACCTAGAGATC
CTCATCCTCGATGCCAATGACAATGCACCCAGTTTCTGTGGGATTTCTACAGGGTTCCATCTTTGAGGATGCTCCACC
CTCGACCAGCATCCTCCAGGTCTCTGCCACGGACCGGACTCAGGTCCCAATGGGCGTCTGCTGTACACCTTCCAGGGTG
GGGACGACGGCGATGGGGACTTCTACATCGAGCCACGTCCGGTGTGATTTCGACCCAGCCCGGCTGGACCGGGAGAAT
GTGGCCGTGTACAACCTTTGGGCTCTGGCTGTGGATCGGGGACGTCCCACTCCCTTAGCGCTCGGTAGAAATCCAGGT
GACCATCTTGGACATTAATGACAATGCCCCATGTTTGGAGAAGGACGAACTGGAGCTGTTTGTGAGGAGAACAACCCAG
TGGGGTTCGGTGGTGGCAAAGATTCTGTGCTAACGACCCGTGATGAAGGCCCTAATGCCAGATCATGTATCAGATTGTGGAA
GGGGACATGCGGCATTTCTTCCAGCTGGACCTGCTCAACGGGACCTGCGTGCCATGGTGGAGCTGGACTTTGAGGTCCG
GCGGGAGTATGTGCTGGTGGTGACAGGCCACGTGCGCTCCGCTGGTGAGCCGAGCCACGGTGACATCCTTCTCGTGGACC
AGAATGACAACCCGCTGTGCTGCCCCGACTTCCAGATCCTCTTCAACAACATATGTACCAACAAGTCCAACAGTTTCCCG
ACCGCGTGATCGGCTGCATCCCGGCCCATGACCCCGACGTGTGACACAGCCTCAACTACACCTTCTGTGACGGGCAACGA
GCTGCGCGTGTGTGCTGCTGACCCCGCCAGACTGCAGCTCAGCCCGGACCTGGACAACAACCGGCCCGTGGAGG
CGCTCATGGAGGTGTCTGTGCTGTGATGGCATCCACAGCTCAGCGCCTTCTGACACCTTCCGTGACCATCATCACGGAC
GACATGCTGACCAACAGCATCACTGTCCGCTGGAGAAGATGTCCAGGAGAAGTTCTGTCCCGCTGTGTGGCCCTCTT
CGTGGAGGGGGTGGCCGCGCTGCTGTCCACCACCAAGGACGACGTCTTCTGCTTCAACGTCCAGAACGACACCGACGTCA
GCTCCAACATCCTGAACGTGACCTTCTCGGCGCTGTGCTGCGCGGCTCCGCGGCCAGTTCTTCCCGTGGAGGACCTG
CAGGAGCAGATCTACCTGAATCGGACGCTGCTGACCACCATCTCCACGACGCGCTGCTGCCCTTCGACGACAACATCTG
CCTGCGCGAGCCCTGCGAGAACTACATGAAGTGGTGTCCGTTCTGCCATTGACAGCTCCGCGGCCCTTCTCAGCTCCA
CCACCGTGTCTTCCCGGCCATCCACCCCATCAACGGCTGCGCTGCCGCTGCCCGCCCGGCTTACCGGGGACTACTGC
GAGACGGAGATCGACCTCTGCTACTCCGACCCGTGCGGCCCAACGGCCGCTGCCCGACCGCGAGGGCGGCTACACCTG
CGAGTGCTTCGAGGACTTCACTGGAGAGCACTGTGAGGTGGATGCCCGCTCAGGCGCGCTGTGCCAACGGGGTGTGCAAGA
ACGGGGGACACCTGCGTGAACCTGCTCATCGGCGCTTCCACTGCGTGTGTCTCTTGGCGAGTATGAGAGGCCCTACTGT
GAGGTGACCAACAGGAGCTTCCCGCCCAAGCTCTTCTGCTCACCCTTCCGGCGCTGAGACAGCGCTTCCACTTACCATCTC
CCTCAGCTTTGCGACTCAGGAAAGCAACGGCTTGTCTTCTACAAACGGCGCTTCAATGAGAAGCAGCACTTCATCGCCC
TGGAGATCGTGGACGAGCAGGTGCAGCTCACCTTCTTGCAGCGAGACAACAACAGCTGGCACCGAAGTTCCCACT
GGTGTGAGTGACGGGCGGTGGCACTCTGTGCAGGTGCACTACTACAACAAGCCCAATATGGCCACCTGGGGCTGGCCCA
TGGGCCGTCCGGGGAAAAGATGGCCGTGGTGACAGTGGATGATTGTGACACAACCATGGCTGTGCGCTTTGGAAGGACA
TCGGGAATAACAGCTGCGCTGCCAGGGGACTCAGACCGCTCCAAGAAGTCCCTGGATCTGACCGGCCCTTACTCCTG
GGGGGTGTCCCAACCTGCCAGAAGACTTCCAGTGACAAACGGCGAGTTCTGTGGGTGCATGCGGAACCTGTGAGTGA
CGCAAAAATGTGGACATGGCCGATTTCATCGCCAACAATGGCAACCGGGAGGCTGCGCTGCTCGGAGGAACCTTCTGCG
ATGGGAGGCGGTGTGAGAATGGAGGCACCTGTGTCAACAGGTGGAATATGTATCTGTGTGAGTGTCCACTCCGATTCCGC
GGGAAGAACTGTGAGCAAGCCATGCTCACCCTCAGCTCTTTCAGCGGTGAGAGCGTCTGTGCTTGGAGTGACCTGAACAT
CATCATCTCTGTGCCCTGGTACCTTGGGGCTCATGTTCCGACCCCGGAAGGAGGACAGCGTTCTGATGGAGGCCACCAGTG
GTGGCCCCACGAGCTTTCGCTCCAGATCCTGAACAACTACCTCCAGTTTGAAGTGTCCACGGCCCCCTCCGATGTGGAG
TCCGTGATGCTGTCCGGTGTGCGGGTGACCGACGGGAGTGGCACCACTTGTGATCGAGCTGAAGAATGTTAAGGAGGA
CAGTGAGATGAAGCACCTGCTCACCATGACCTTGGACTATGGGATGGACCGAGACAAGGCAGATATCGGGGACATGCTTC
CCGGGCTGACGGTAAGGAGCGTGGTGGTGGAGGCGCTCTGAAGACAAGGTCTCCGTGCGCGGTGGATTCCGAGGCTGC
ATGCAGGGAGTGGAGTGGGGGGGACGCCACCAACGTGCGCACCTTGAACATGAACAACGCACTCAAGGTGAGGCTGAA
GGACGGCTGTGATGTGGACGACCCCTGTACCTCGAGCCCTGTCCCCCAATAGCGCTGCCACGACGCTTGGAGGACT
ACAGCTGCGTCTGTGACAAAGGGTACCTTGGAAATAACTGTGTGGATGCTGTACCTGAACCCCTGCCAGAACATGGGG
GCCTGCGTGGCTCCCCCGGCTCCCCGACGGGCTACGTGTGCGAGTGTGGGCCCAAGTCACTACGGGCCGTACTGTGAGAA
CAAACCTGACCTTCCGTGCCCCAGAGGCTGGTGGGGGAACCCCGCTCTGTGGACCTTGCACCTGTGCCGTGACCAAGGCT
TTGATCCCGACTGTAAATAAGACCAACGGCCAGTGCCAATGCAAGGAGAATTACTACAAGCTCCTAGCCCAGGACACCTGT
TGCCCTTGCAGCTGCTTCCCCATGGCTCCCCACCGGCACTTGGCAGATGGCCACCGGGCAGTGTGCTGCAAGCCCGG
CGTCATCGGCCGCCAGTGTGCAACCGCTGCGACAACCCGTTTGCCGAGGTACCAACGCTCGGCTGTGAAGTGATCTACAATG
GCTGTCCCAAAGCATTTGAGGCGGGCATCTGTGTGGCCACAGACCAAGTTCCGGCAGCGCGCTGCGCTGCCATGTCCATTAAG
GGATCCGTGGAAATGCGGTCCGACACTGCAGCGGGGAGAAGGGCTGGCTGCCCGCAGAGCTCTTTAACTGACCCACCAT
CTCCTTCTGTGACCTCAGGGCATGAATGAGAAGCTGAGCCGCAATGAGACGAGGTGGACGGCGCCAGGCGCTGACAG
TGGTGAGGGCCCTTCCGAGTGTACACAGCACACGGGCACGCTCTTTGGCAATGAGTGGCGACGGCTTACCAGCTGTGTG
GGCCACGTCCTTTCAGCACGAGAGCTGGCAGCAGGGCTTTCACCTGGCAGCCACGAGGACGCGACTTTACAGGAGCGT
CATCCACTCGGGCAGCGCCCTCTTGGCCCCAGCCACCAGGGCGCGCTGGGAGCAGATCCAGCGGAGCGAGGGCGGCACGG
CACAGCTGCTCCGGCGCTCGAGGGCTACTTTCAGCAACGTGGCACCAACGTGCGGCGGACGTACCTGCGGCCCTTCTGTC
ATCTGTCACCGCAACATGATTTCTGTGTCGACATCTTTGACAAGTTCAAACCTTACGGGAGCCAGGCTCCCCGCTTTCGA
CACCATCCATGAAGAGTTCCCGAGGAGACTGGAGTCTCCGCTCTCCTTCCACGCGACTTCTTCAGACCACTTAAACCCCGA
AAGAAGGCCCCCTGCTGAGGCGGGCTGGCCGGAGGACCAACCCGAGCCACGCGCCCGGGGCTGGCACCGAGAGGGAG
GCCCCGATCAGCAGGCGGAGGCGACACCTGATGACGCTGGCCAGTTGCGGCTGCTGCTGCTCATCATTTACACCACTT
GGGGCAGCTCCTGCCCCGAGGCTACGACCCCGACCGTCCGAGCTTCCGTTGGCTTACCGGCCCATTAATACCCCGA
TGGTGACACGCTGCTGTACAGCGAGGGGCTCCGCTCCCGAGACCCCTGGAGAGGGCCGCTCGGTGGAGTTTCGCCCTG
CTGGAGGTGGAGGAGCGAACCAAGCTGTCTGCTGCTTCTGGAACCACTCCCTGGCCGTGGTGGGACGGGAGGGTGGTC

FIG. 1 Continued

TGCCCCGGGGCTGCGAGCTCCTGTCCAGGAACCGGACACATGTCCCTGCCAGTGCAGCCACACAGCCAGCTTTGCGGTGC
TCATGGATATCTCCAGGCGTGAGAACGGGGAGGTCCCTGCCCTCTGAAGATTGTACCTATGCCGCTGTGTCTTTGTCACCTG
GCAGCCCTGCTGGTGGCCCTTCCTCCTCTGAGCCTGGTCCGCATGCTGCGCTCCAACCTGCACAGCATTACAAAGCACCT
CGCCGTGGCGCTCTTCTCTCTCAGCTGGTGTTCGTGATTGGGATCAACCAGACGGAAAACCCGTTTCTGTGCACAGTGG
TTGCCATCTCCTCCACTACATCTACATGAGCACCTTTGCCTGGACCTTCGTGGAGACCTGCATGTCTACCGCATGCTG
ACCGAGGTGCGCAACATCGACACGGGGCCCATGCGGTTCTACTACGTGCTGGGCTGGGGCATCCCGGCCATTGTACAGG
ACTGGCGGTGCGCCTGGACCCCCAGGGCTACGGGAACCCCGACTTCTGCTGGCTGTGCTTCAAGACACCCCTGATTTGGA
GCTTTGCGGGGGCCCATCGGAGCTGTTATAATCATCAACACAGTCACTTCTGTCTTATCTGCAAAGGTTTCTGCCAAAGA
AAGCACCATTAATTATGGGAAAAAAGGGATCGTCTCCCTGCTGAGGACCGCATTCCTCCTGCTGCTGCTCATCAGCGCCAC
CTGGCTGCTGGGGCTGCTGGCTGTGAACCGCGATGCACTGAGCTTTCACTACCTCTTCGCCATCTTCAGCGGCTTACAGG
GCCCTTCTGCTCCTCTTTTCCACTGCGTGTCTCAACCAGGAGGTCCGGAAGCACCTGAAGGGCGTCTCGGCGGGAGGAAG
CTGCACCTGAGGACTCCGCCACCACCAGGGCCACCCTGCTGACGCGCTCCCTCAACTGCAACACCCACTTCGGTGACGG
GCCTGACATGCTGCGCACAGACTTGGGCGAGTCCACCGCTCGCTGGACAGCATCGTCAGGGATGAAGGGATCCAGAAGC
TCGGCGTGTCTCTGGGCTGGTGAGGGGCAGCCACGGAGAGCCAGACGCTCCCTCATGCCCAGGAGCTGCAAGGATCCC
CCTGGCCACGATTCCGACTCAGATAGCGAGCTGTCCCTGGATGAGCAGAGCAGCTCTTACGCCCTCCTCACACTCGTCAGA
CAGCGAGGACGATGGGGTGGGAGCTGAGGAAAAATGGGACCCGGCCAGGGGGCGCCCTCCACAGCACCCCCAAAGGGGACG
CTGTGGCCAACCACTTCCGGCCGGCTGGCCCGAACCAGAGCCTGGCTGAGAGTGACAGTGAGGACCCAGCGGCAAGCCC
CGCTTGAAGGTGGAGACCAAGGTCAGCGTGGAGCTGCACCGCGAGGAGCAGGGCAGTCACCGTGGAGAGTACCCCCGGA
CCAGGAGAGCGGGGGCGCAGCCAGGCTTGCTAGCAGCCAGCCCCAGAGCAGAGGAAAGGCATCTTGAATAAAGTCA
CCTACCCCGCCCGCTGACGCTGACGGAGCAGACGCTGAAGGGCCGGCTCCGGGAGAAGCTGGCCGACTGTGAGCAGAGC
CCCACATCTCGCCACGCTCTTCCCTGGGCTCTGGCGGGCCCCGACTGCGCCATCACAGTCAAGAGCCCTGGGAGGGAGCC
GGGGCGTGACCACCTCAACGGGGTGGCCATGAATGTGCGCACTGGGAGCCCCAGCCGATGGCTCCGACTCTGAGAAAC
CGTGA

FIG. 2

MAPPPPPVLPVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPCTYAVGAACPAPRELLDVGRDGRLAGRRRVSS
 GAGRPLPLQVRLVARSAPTALSRRRLRARTHLPGCGARARLCGTGARLCCGALCFPVPGGCAAAQHSALAAPTTL PACRCPP
 RPRPRCPGRPICLPFGGSVRLRLLCALRAAGAVRVGLALEAATAGTFSASPSPPSPPLPPNLPEARAGPARRARRCTSGR
 GSKFPMPNYQVALFENEPAATLILQLHAHYTIEGEEERVSYMEGLFDESRGRYFRIDSATGAVSTDSVLDRETKETHV
 LRVKAVDYSTPPRSATTYITVLVKDINDHSPVFEQSEYREVRRENLEVGYEVLITIRASDRDSPINANLRYRVLGGAWDVF
 QLNESSCVVSTRAVLDRREEAAEYQLLVEANDQGRNPGLSATATVYIEVEDENDNYPQFSEQNYVVOVPEIDVGLNTAVLR
 VQATDRDQGGNAAIHYSILSGNVAGQFYLHSLSGILDVINPLDFEDVQKYSLSIKAQDGRPPLINSSGVVSVQVLDVND
 NEPIFVSSPFQATVLENVPLGYPVVHIQAVDADSGENARLHYRLVDTASTFLGGGSAGPKNPAPTDFPFQIHNSSGWIT
 VCAELDREEVEHYSGVEAVDHGSPFMSSTSVSITVLDVNDNDVFTQPTYELRLNEDAAGSSVLTQLQARDRANSVI
 TYQLTGNTNRNRFALSSQRGGGLITLALPLDYKQEQQYVLAVTASDGTSTRHTAHVLINVTANTRHPVQSSHYTVSVSE
 DRFVGTSIATLSANDEDTGENARITYVIQDPVPQFRIDPDSGTMYTMMELDYENQVAYTLTMAQDNGIPQKSDTTTLEI
 LILDANDNAPQLWDFYQGSIFEDAPPSTSLQVSATDRDSCPNORLLYTFQGGDDGDCDFYIEPTSGVIRTRRLDREN
 VAVYNLWALAVDRGSPPTLSASVEIQVTILDINDNAPMEFEKDELELFEENNPFVGSVAKIRANDPEDEGNAQIMYQIVE
 GDMRHFFQLDLLNGDLRAMVELDFEVRREYVLVVQATSAPLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTNKSNSFP
 TGVIGCTPAHDPDVSLSNYTTFVQGNELRLLLLDPATGELQLSRDLDMNRPLEALMEVSVSDGIHSVTAFCTLRVTIITD
 DMLTNSITVRLENMSQEKFLSPLLALFVEGVA AVLSTTKDDVFVFNQNDTDVSSNINLVTF SALLPGGVRGQFFPSEDL
 QEQIYLNRITLTITISTQRVLPFDNCLREPCENYMKCVSVLRFDPSSAPFLSSTTVLFRPIHPINGLRRCRCPPGFTGQYC
 ETEIDL CYSDPCGANGRCRCSREGGYTCECFEDFTGEHCEVDARSGRCANGVCKNGGTCVNLLIGGFHCVCPPGEYERPYC
 EVTTRSPFPQSVFTRGLRQRHFHTISLTFATQERNGLLYNGRNFNEKHDFIALEIVDEQVQLTF SAGETTTTVAPKVPFS
 GVS DGRWHSVQVOYNNKPNIGHLPLPHGSPGKMAVTVDDCDTMAVRFGKDIGNYSCAAQQTQTGSKKSLDLTGPLLL
 GGVPNL PEDFPVHNRRQFVGCMRNLSDGKNVDMAGFIANNGTREGCAARRNFC DGRRCONGGTCVNRWNMYLCECPLRFG
 GKNCEQAMPHPQLFSGESVVSWSDLNIIISVPWYLGMLFRTRKEDSVLMEATSGGPTSFRLLQILNNYLQFEVSHGPSDVE
 SVMLSGLRVTDGEWHLLIELKNVKEDSEM KHLVTMTLDYCMDQNKADIGGMLPGLTVRSVVVGASEDKVSVRRGFRGC
 MQGVRMGCTPTNVATLNMNNAKVRVKDGCDDVDPCTSSPCPPNSRCHDAWEDYSCVCDKGYLGINCV DACHLNPCENMG
 ACVRSPGSPQGYVCECGPSHYGPYCENKLDLPCPRGWGNPNVCGPCHCAVSKGFPDPCNKTNQCCQCKENYKLLAQDTC
 LPCDCFPHGSHSRCTCDMATGQCACKPGVIGRQCNRCDNPF AEVTTLGCEVTYNGCPKAFEAGIWWPQTKFGQPAAVPCPK
 GSVGNAVRHCSGEGKWLPELFNCTTISFVDLRAMNEKLSRNETQVDGARALQLVRLRSATQHTGTLPNDVVRTAYQLL
 GHVLQHESWQQGFDLAATQDADFHEVDI HSGSALLAPATRAAWEQIQRSEGCTAQLLRLECYFSNVARNVRRTYLRPFV
 IVTANMILAVDIFDKFNFTGARVPRFDTHIEEFPRELESSVSFPADFFRPPEEKEGPLL RPAGRRTPQTTRPGPGTERE
 APISRRRRHPDDAGQFAVALVIIYRTLQOLLPERYDPDRSLRLPHRPIINTPMVSTLVYSECAPLPRPLERFVLVEFAL
 LEVEERTKPVCFWNHSLAVGGTGGWSARGCELLSRNRTHVACQCSHTASEAVLMDISRRENGEVLPLKIVTYAAVSLSL
 AALLVAFVLLSLVRMLRSNLHSIHKHLAVALFLSQLVFVIGINQ TENEFLLCTVVAILLHYIYMSTFAWTLVESLHVYRML

TEVRNIDTGPMRFYYVVGWGIPIAVTGLAVGLDPQGYGNPDFCWLSQLDTLIWSFAGPIGAVIIINTVTSVLSAKVSCQR
 KHHYYGKKGIVSLRLTAFLLLLLISATWLLGLLAVNRDALSFHYLFAIFSGLQGPVLLFHCVLNQEVRKHLKGVLGGRK
 LHLEDSATTRATLLTRSLNCTTFGDPMLRTDLGESTASLDSIVRDEGIQKLGVS SGLVRGSHGEPDASLMFRSCKDP
 PQHDSDSSELSLDEQSSSYASSHSSDSEDDGVGAEEKWDPARGAVHSTPKGDAVANHPAGWPDQSLAESDSEDPSGKP
 RLKVETKVSVELHREBQGS HRGEYPPDQESGCAARLASSQPPEQRKGILKNKVYPPPLTLTEQTLKGRLEKLADCEQS
 PTSSRTSSLGSGGPDCAITVKSPPGREGDHLNGVAMNVRTGSAQADGSDSEKP

FIG. 3

Score = 939 (140.9 bits), Expect = 4.0e-81, Sum P(3) = 4.0e-81
Identities = 203/218 (93%), Positives = 203/218 (93%), Strand = Plus / Plus

Query: 230 CTGTAATAAGACCAACGGCCAGTGCCAAT-GCAAGGAGAATTACTACAAGCTCCTAGCCC 288
CTG A T A A C GCC TG C T QCA GGAGAATTACTACAAGCTCCTAGCCC
Sbjct: 38281 CTGAAGTCACAGGCCCTGCCTCTGGCTTTTGCA-GGAGAATTACTACAAGCTCCTAGCCC 38339

Query: 289 AGGACACCTGTCTGCCCTGGGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA 348
AGGACACCTGTCTGCCCTGGGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA
Sbjct: 38340 AGGACACCTGTCTGCCCTGGGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA 38399

Query: 349 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGCGTCATCGGCCGCCAGTGCAACCGCTGCG 408
TGGCCACCGGGCAGTGTGCCTGCAAGCCCGCGTCATCGGCCGCCAGTGCAACCGCTGCG
Sbjct: 38400 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGCGTCATCGGCCGCCAGTGCAACCGCTGCG 38459

Query: 409 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 447
ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG
Sbjct: 38460 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 38498

FIG. 4

Score = 1000 (352.0 bits), Expect = 2.4e-98, P = 2.4e-98
Identities = 162/186 (87%), Positives = 172/186 (92%), Frame = +3

Query: 3 YLGINCVDACHLNPENMGACVRSPGSPQGYVCECGFSHYGPYCENKLDLPCPRGWWGNP 182
Y G CVDAC LNPC+++ ACVRSP +P+GY CECGP HYG YCENK+DLPCP+GWWGNP
Sbjct: 1917 YFGKKCVDACLLNPCKHVAACVRSPNTPRGYSCECGPGHYGYCENKVDLPCPKGWWGNP 1976

Query: 183 VCGPCHCAVSKGFDPCNKTNQGQCCKENYYKLLAQDTCLPCDCFPHGSHSRTCDMATGQ 362
VCGPCHCAVS+GFDPCNKTNQGQCCKENYYK AQD CLPCDCFPHGSHSR CDM TGQ
Sbjct: 1977 VCGPCHCAVSQGFDPCKTNKGQCCKENYYKPPAQDACLPDCFPHGSHSRACDMDTGQ 2036

Query: 61 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCCAGTCACT 120
|||||
Sbjct: 33445 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCCAGTCACT 33504

Query: 121 ACGGGCCGTACTGTGAGAACAA 142
|||||
Sbjct: 33505 ACGGGCCGTACTGTGAGAACAA 33526

FIG. 5

Score = 12924 (4549.5 bits), Expect = 0.0, P = 0.0
 Identities = 2451/3034 (80%), Positives = 2677/3034 (88%)

Query: 1 MAPPPFPVLPVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPGCTYAVGAACTPR- 59
 MAP P VLP L+LLAAAA LPA+ L AAWE RVPGG RAFAL PG +Y + TPR

Sbjct: 1 MAPSSPRVLPALVLLAAAA-LPALELGAAAWELRVPGGARAFALGPGWSYRLDTTRTPRE 59

Query: 60 ---APRELLDVGRD-GRLAGRRRVSG-AGRPLPLQVRLVARSAFTALSRRLRARTHLPGC 114
 RE GR G AG + AGR LPLQVRLVAR APTA S LRAR + C

Sbjct: 60 LLDVSREGPAAGRRLGLGAGTLGCARLAGRLLEPLQVRLVARGAFTAPSLVLRARAYGARC 119

Query: 115 GARA-RLCGTGARL-----CG-ALCFVPGGCAAAQHSALAAPTTLPACRCPPRP 162
 G R R GA L G ALCFP GG AA+ S L A T PAC CPP

Sbjct: 120 GVRLRRSARGAELRSPAVRSVPGLGDALCFPAAGGGAASLTSVLEAITNFPACSCPPVA 179

Query: 163 RPRCPGRPICLPFGGSVRLRLCALRRAAGAVRVGLALEAATAGTPSASPSPPPLPPNL 222
 C PICL PGGS LRL+CAL RAAGAV V L ++A T+GTPS SPS SP L NL

Sbjct: 180 GTGCRRGPICLRPGSAELRLVLCALGRAAGAVVVELVIQA-TSGTPSESFSVSPSLL-NL 237

Query: 223 PEARAGPARRARRGTSGRGSLKFFMPNYQVALFENEPAGTLILQLHAHYTIEGEEERSVY 282
 + RAG RR+RRGT S +FP+P+YQV++ ENEPAGT +++L AH EG+ R+SV

Sbjct: 238 SQPRAGVVRRSRRCTGSSTSPQFPLPSYQVSVPENEPAGTAVIELRAHDPDEGDAGRLSY 297

Query: 283 YMEGLFDESRGYFRIDSATGAVSTDSVLDRETKETHVLRVKAVDYSTPPRSATTYITVL 342
 ME LFDERS GYF ID+ATGAV+T LDRETK+THVL+V AVD+ +P RSA TY+TV

Sbjct: 298 QMEALFDESRNGYFLIDAATGAVTTARSLDRETKDTHVLKSAVDHGSPPRRSAATYLTVT 357

Query: 343 VKDTNDHSPVFEQSEYRERRENLEVGVEVLTIRASDRDSPINANLRYRVLGGAWDVFLQ 402
 V DTNDHSPVFEQSEYRER+RENLEVGVEVLTIRA+D D+P NAN+RYR+L GA VF++

Sbjct: 358 VSDTNDHSPVFEQSEYRERIRENLEVGVEVLTIRATDGDAPSNANMRYRLLEGAGGVFEI 417

Query: 403 NESSGVVSTRAVLDRREEAAYQLLVEANDQGRNPGPLSATATVYIEVEDENDNYPQFSEQ 462
 + SGVV TRAV+DREEAAYQLLVEANDQGRNPGPLSA+ATV+I VEDENDNYPQFSE+

Sbjct: 418 DARSGVVRTRAVVDREEAAYQLLVEANDQGRNPGPLSASATVHIVVEDENDNYPQFSEK 477

Query: 463 NYVVQVPEDVGLNTAVLRVQATDRDQGNAAIHYSILSGNVAGQFYLHSLSGILDVINPL 522
 YVVQVPEDV +NTAVLRVQATDRDQGNAAIHYSI+SGN+ GQFYLHSLSG LDVINPL

Sbjct: 478 RYVVQVPEDVAVNTAVLRVQATDRDQGNAAIHYSIVSGNLKGQFYLHSLSGSLDVINPL 537

Query: 523 DFEDVQKYSLSIKAQDGRPPLINSSGVSVQVLDVNDNEPIFVSSPFQATVLENVPLGY 582
 DFE +++Y+L IKAQDGRPPLINSSG+VSVQVLDVNDN PIFVSSPFQA VLENVPLG+

Sbjct: 538 DFEAIREYTLRIKAQDGRPPLINSSGLVSVQVLDVNDNAPIFVSSPFQAAVLENVPLGH 597

Query: 583 PVVHIQAVDADSGENARLHYRLVDTASTFLGGGSAGPKNPAPTDFPFQIHNSSGWITVC 642
 V+HIQAVDAD+GENARL YRLVDTAST +GG S +NPA PDFPFQIHNSSGWITVC

Sbjct: 598 SVLHIQAVDADAGENARLQYRLVDTASTIVGGSSVDSNPASAPDFPFQIHNSSGWITVC 657

Query: 643 AELDREEVEHYSGVEAVDHGSPPMSSSTSVSITVLDVNDNDFVFTOPTYELRLNEDAAV 702
 AELDREEVEHYSGVEAVDHGSP MSSS SVSITVLDVNDNDP+FTQP YELRLNEDAAV

Sbjct: 658 AELDREEVEHYSGVEAVDHGSPAMSSSASVSITVLDVNDNDPMFTQPVYELRLNEDAAV 717

Query: 703 GSSVLTLOARDRDANSVITYQLTGGNTRNRFALSSQGGGLITLALPLDYKQEQQYVLAV 762
 GSSVLT+L+ARDRDANSVITYQLTGGNTRNRFALSSQ GGGLITLALPLDYKQE+QYVLAV

Sbjct: 718 GSSVLTLRARDRDANSVITYQLTGGNTRNRFALSSQSGGLITLALPLDYKQERQYVLAV 777

Query: 763 TASDGTRSHTAHVLINVTANTRHPVFQSSHYTVSVSEDRPVGTSIATLSANDEDTGENA 822
 TASDGTRSHA V INVTANTRHPVFQSSHYTVSVSEDRPVGTSIAT+SA DEDTGENA

Sbjct: 778 TASDGTRSHAQVFINVTANTRHPVFQSSHYTVSVSEDRPVGTSIATISATDDEDTGENA 837

Query: 823 RITYVIQDPVPQFRIDPDSGTYMTMELDYENQVAYTLTMAQDNGIPQKSDTTTLEILI 882
 RITYV++DPVPQFRIDP+GT+YTM ELDYE+Q AYTL I AQDNGIPQKSDTT+LEILI

Sbjct: 838 RITYVLEDVPVPQFRIDPDTGTIYTMELDYEDQAAYTLAITAQDNGIPQKSDTTTLEILI 897

FIG. 5 Continued

Query: 883 LDANDNAPQFLWDFYQGSIFEDAPPSTSILOVSATDRDSGPNGRLLYTFQGGDDGDGDFY 942
LDANDNAP+FL DFYQGS+FEDAPPSTS+LOVSATDRDSGPNGRLLYTFQGGDDGDGDFY

Sbjct: 898 LDANDNAPRFLRDFYQGSVFEDAPPSTSVLQVSATDRDSGPNGRLLYTFQGGDDGDGDFY 957

Query: 943 IEPTSGVIRTQRRLDRENNAVYNLWALAVDRGSP TPLSASVEIQVTILDINDNAPMFEKD 1002
IEPTSGVIRTQRRLDRENNAVYNLWALAVDRGSP PLSASV IQV++LDINDN P+FEKD

Sbjct: 958 IEPTSGVIRTQRRLDRENNAVYNLWALAVDRGSPNPLSASVGIQVSULDINDNPPVFEKD 1017

Query: 1003 ELELFVEENNFPVGSVVAKIRANDPDEGPNQAIYQIVEGDMRHHFQLDLLNGDLRAMVEL 1062
ELELFVEEN+PVGSVVA+IRANDPDEGPNQAI+YQIVEG++ FQLDLL+GDLRA+VEL

Sbjct: 1018 ELELFVEENSPVGSVVARIRANDPDEGPNQAIYQIVEGNVPEVFQLDLLSGDLRALVEL 1077

Query: 1063 DFEVRREYVLVQATSAPLVSRA TVHILLVDQNDNPPVLPDFQILFN NYVTNKSNSFPPTG 1122
DFEVR+Y+LVVQATSAPLVSRA TVHI L+QNDNPP LPDFQILFN NYVTNKSNSFP+G

Sbjct: 1078 DFEVRDYMLVQATSAPLVSRA TVHIRLLDQNDNPPVLPDFQILFN NYVTNKSNSFP+G 1137

Query: 1123 VIGCIPAHDPDVS DLSNYTFVQGNELRLLLLD PATGELQLSRDL DNNRPLEALMEVSVSD 1182
VIG IPAHDPD+SDLSNYTF+QGNEL LLLLD PATGELQLSRDL DNNRPLEALMEVSVSD

Sbjct: 1138 VIGRIPAHDPDLSDLSNYTFVQGNELSLLLLD PATGELQLSRDL DNNRPLEALMEVSVSD 1197

Query: 1183 GIHSVTAFCTLRVTIITDDMLTNSITVRLENMSQEKFLSP LLLALFVEGVAAVLSTTKDDV 1242
GIHSVTA CTLRVTIITDDMLTNSITVRLENMSQEKFLSP LL+LFVEGVA VLSTTKDD+

Sbjct: 1198 GIHSVTALCTLRVTIITDDMLTNSITVRLENMSQEKFLSP LLSLFVEGVATVLSTTKDDI 1257

Query: 1243 FVFNVDNDTDVSSNILNVTF SALLPGGV RGQFFPSED LQEQIYLNRTLLTTISTQ RVLPF 1302
FVFN+QNDTDVSSNILNVTF SALLPGG RG+FFPSED LQEQIYLNRTLLTTIS QRVLPF

Sbjct: 1258 FVFNVDNDTDVSSNILNVTF SALLPGGTRGRFFPSED LQEQIYLNRTLLTTISAQ RVLPF 1317

Query: 1303 DDNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHP INGLRCRCPPGFTGDYCET 1362
DDNICLREPCENYMKCVSVLRFDSSAPF+SSTTVLFRPIHPI GLRCRCPPGFTGDYCET

Sbjct: 1318 DDNICLREPCENYMKCVSVLRFDSSAPFISSTTVLFRPIHPITGLRCRCPPGFTGDYCET 1377

Query: 1363 EIDL CYSDPCGANGRCRSREGGYTCECFEDFTGEHC EVDARSGRCA NGVCKNGGTCVNLL 1422
EIDL CY+S+PCGANGRCRSREGGYTCECFEDFTGEHC+V+ RSGRCA+GVCKNGGTCVNLL

Sbjct: 1378 EIDL CYSNPCGANGRCRSREGGYTCECFEDFTGEHCQVNRSGRCASGVCKNGGTCVNLL 1437

Query: 1423 IGGFHCVCPPGEYERPYCEVTRSFPPQSFVTFRGLRQRFHFTISLTFATQERNGLLLYN 1482
IGGFHCVCPPGEYE PYCEV+TRSFPPQSFVTFRGLRQRFHFT+SL FATQ+RN LLLYN

Sbjct: 1438 IGGFHCVCPPGEYEHYPYCEVSTRSFPPQSFVTFRGLRQRFHFTVSLAFATQDRNALLYN 1497

Query: 1483 GRFNEKHDFIALEIVDEQVQLTFSAGETTTTVAPKVP SGVSDGRWHSVQVQYYNKPNIGH 1542
GRFNEKHDFIALEIV+EQ+QLTFSAGETTTTV P+VP GVSDGRWHSV VQYYNKPNIGH

Sbjct: 1498 GRFNEKHDFIALEIVREQVQLTFSAGETTTTVTPQVGGVSDGRWHSVLVQYYNKPNIGH 1557

Query: 1543 LGLPHGSPSGEKMAVVTDDCDTMAVRFGKDIGNYSCAAQGTQTGSKKSLDLTG PLLLGG 1602
LGLPHGSPSGEK+AVVTDDCD +AV FG +GNYSCAAQGTQ+GSKKSLDLTG PLLLGG

Sbjct: 1558 LGLPHGSPSGEKVAVVTDDCDAVAVHFGSYVGNYSCAAQGTQSGSKKSLDLTG PLLLGG 1617

Query: 1603 VPNLPEDFPVHNRQFVGCMRNL SVDGKNVDMAGFIANNGTREGCAARRNFC DGRRCQNGG 1662
VPNLPEDFPVH+RQFVGCMRNL S+DG+ VDMA FIANNGTR GCA++RNFC DGRRCQNGG

Sbjct: 1618 VPNLPEDFPVHNRQFVGCMRNL SIDGRIVDMAAF IANNGTRAGCASQRNFC DGTSCQNGG 1677

Query: 1663 TCVNRWNMYLCECPLRFGGKNCEQAMPHPQLFSGESVVSWSDLNIIISVPWYLGLMFRTR 1722
TCVNRWN YLCECPLRFGGKNCEQAMPHPQ F+GESVV WSDL+I ISVPWYLGLMFRTR

Sbjct: 1678 TCVNRWNTYLCECPLRFGGKNCEQAMPHPQRFTGESVVLWSDLDITISVPWYLGLMFRTR 1737

FIG. 5 Continued

Query: 2563 VRNIDTGPMRFYYVVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGFIGAV 2622
VRNIDTGPMRFY+VVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGP+G V

Sbjct: 2578 VRNIDTGPMRFYHVVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGPVGTV 2637

Query: 2623 IIINTVTSVLSAKVSCQRKHHYVYGGKGVSLRLTAFLLLLLISATWLLGLLAVNRDALS 2682
IIINTV VLSAKVSCQRKHHY +KG+VS+LRTAFLLLLL++ATWLLGLLAVN D LSF

Sbjct: 2638 IIINTVIFVLSAKVSCQRKHHYERKGVVSMRLTAFLLLLLVTATWLLGLLAVNSDTLSF 2697

Query: 2683 HYLFAIFSGLQGPVLLFHCVLNOEVRKHLKGVLCGRKLHLED SATTRATLLTRSLNCNT 2742
HYLFA FS LQG FVLLFHCV ++EVRKHL+ VL G+KL L+DSATTRATLLTRSLNCN

Sbjct: 2698 HYLFAAFSCLQGFVLLFHCVAHREVRKHLRAVLAKKKQLD DSATTRATLLTRSLNCNN 2757

Query: 2743 TFGDGPDMRLRTDLGESTASLDSIVRDEGIQKLGVS SGLVRGSHGEPDASLMPRSCKDPPG 2802
T+ +GPDMLRT LGESTASLDS RDEG+QKL VSSG RG+HGEPD S +PR+ K G

Sbjct: 2758 TYSEGPDMLRTALGESTASLDSSTRDEGVQKLSVSSGPARGNHGEPDTSFIPRNSKKAHG 2817

Query: 2803 HDSDSDSEL SLDEQSSSYASSHSDSEDDGVGAEEKWD PARGAVHSTPKGDAVANHVPA 2862
DSDSDSEL SLDE SSSYASSH+SDSEDDG AE+KW+PA G HSTPK DA+ANHVPA

Sbjct: 2818 PDSDSDSEL SLDEHSSSYASSHTSDSEDDGGEAEDKWNPA GGPAGHSTPKADALANHVPA 2877

Query: 2863 WPDQSLAESDSEDPGKPRKLVETKVSVELHREEQSGHRGEYPPDQESGGAAR---LASS 2919
WPD+SLA SDSE+ +P LKLVETKVSVELHR+ QG+H G+ P D ESG A+ + SS

Sbjct: 2878 WPDES LAGSDSEELDT EPHLKLVETKVSVELHRQAQGNHCGRPSDPESGVLAKPVAVLSS 2937

Query: 2920 QPPEQRKGILKNKVITYPPPLTLTEQTLKGRLREKLADCEQSPTSSRTSSLGSG----GPD 2975
QP EQRKGILKNKVITYPPPL EQ LK RLREKLADCEQSPTSSRTSSLGSG D

Sbjct: 2938 QPQEQRKGILKNKVITYPPPLP--EQPLKSRLREKLADCEQSPTSSRTSSLGSGDGVHATD 2995

Query: 2976 CAITVKSPGREPGRDHLNGVAMNVRTGSAQADGSDSEKP 3014
C IT+K+P REPGR+HLNGVAMNVRTGSAQA+GSDSEKP

Sbjct: 2996 CVITIKTPRREPGRHLNGVAMNVRTGSAQANGSDSEKP 3034

FIG. 6

[illegible]

| DATE | NAME | AMOUNT | DATE | NAME | AMOUNT |
|------|--------|--------|------|------|--------|
| 1890 | John | 100 | 1890 | John | 100 |
| 1891 | John | 100 | 1891 | John | 100 |
| 1892 | John | 100 | 1892 | John | 100 |
| 1893 | John | 100 | 1893 | John | 100 |
| 1894 | John | 100 | 1894 | John | 100 |
| 1895 | John | 100 | 1895 | John | 100 |
| 1896 | John | 100 | 1896 | John | 100 |
| 1897 | John | 100 | 1897 | John | 100 |
| 1898 | John | 100 | 1898 | John | 100 |
| 1899 | John | 100 | 1899 | John | 100 |
| 1900 | John | 100 | 1900 | John | 100 |
| 1901 | John | 100 | 1901 | John | 100 |
| 1902 | John | 100 | 1902 | John | 100 |
| 1903 | John | 100 | 1903 | John | 100 |
| 1904 | John | 100 | 1904 | John | 100 |
| 1905 | John | 100 | 1905 | John | 100 |
| 1906 | John | 100 | 1906 | John | 100 |
| 1907 | John | 100 | 1907 | John | 100 |
| 1908 | John | 100 | 1908 | John | 100 |
| 1909 | John | 100 | 1909 | John | 100 |
| 1910 | John | 100 | 1910 | John | 100 |
| 1911 | John | 100 | 1911 | John | 100 |
| 1912 | John | 100 | 1912 | John | 100 |
| 1913 | John | 100 | 1913 | John | 100 |
| 1914 | John | 100 | 1914 | John | 100 |
| 1915 | John | 100 | 1915 | John | 100 |
| 1916 | John | 100 | 1916 | John | 100 |
| 1917 | John | 100 | 1917 | John | 100 |
| 1918 | John | 100 | 1918 | John | 100 |
| 1919 | John | 100 | 1919 | John | 100 |
| 1920 | John | 100 | 1920 | John | 100 |
| 1921 | John | 100 | 1921 | John | 100 |
| 1922 | John | 100 | 1922 | John | 100 |
| 1923 | John | 100 | 1923 | John | 100 |
| 1924 | John | 100 | 1924 | John | 100 |
| 1925 | John | 100 | 1925 | John | 100 |
| 1926 | John | 100 | 1926 | John | 100 |
| 1927 | John | 100 | 1927 | John | 100 |
| 1928 | John | 100 | 1928 | John | 100 |
| 1929 | John | 100 | 1929 | John | 100 |
| 1930 | John | 100 | 1930 | John | 100 |
| 1931 | John | 100 | 1931 | John | 100 |
| 1932 | John | 100 | 1932 | John | 100 |
| 1933 | John | 100 | 1933 | John | 100 |
| 1934 | John | 100 | 1934 | John | 100 |
| 1935 | John | 100 | 1935 | John | 100 |
| 1936 | John | 100 | 1936 | John | 100 |
| 1937 | John | 100 | 1937 | John | 100 |
| 1938 | John | 100 | 1938 | John | 100 |
| 1939 | John | 100 | 1939 | John | 100 |
| 1940 | John | 100 | 1940 | John | 100 |
| 1941 | John | 100 | 1941 | John | 100 |
| 1942 | John | 100 | 1942 | John | 100 |
| 1943 | John | 100 | 1943 | John | 100 |
| 1944 | John | 100 | 1944 | John | 100 |
| 1945 | John | 100 | 1945 | John | 100 |
| 1946 | John | 100 | 1946 | John | 100 |
| 1947 | John | 100 | 1947 | John | 100 |
| 1948 | John | 100 | 1948 | John | 100 |
| 1949 | John | 100 | 1949 | John | 100 |
| 1950 | John | 100 | 1950 | John | 100 |
| 1951 | John | 100 | 1951 | John | 100 |
| 1952 | John | 100 | 1952 | John | 100 |
| 1953 | John | 100 | 1953 | John | 100 |
| 1954 | John | 100 | 1954 | John | 100 |
| 1955 | John | 100 | 1955 | John | 100 |
| 1956 | John | 100 | 1956 | John | 100 |
| 1957 | John | 100 | 1957 | John | 100 |
| 1958 | John</ | | | | |

FIG. 7

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCCTGGCGCTGGCGCTGGGGCCGGGGTCCGCGGGGGGC
 CACCCTCAGCCGTGCGGGCTCCTGGCGCGCCTCGGGGGCTCCGTGCGCCTGGGCGCCCTCCTGCCCC
 GCGCGCCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCGCCCTGGCGCGCGGCTGCC
 GCACAACCTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCCGCGACCCCGCCTCGCTGACCCGC
 GGCTGTGCCAGGCGCTGGTGCCTCCGGGGCGTGGCGGGCCTGCTCGCCTTTCCCGAGGCTCGGCCCG
 AGCTGCTGCAGCTGCACTTCTGGCGGGCGGCCACCGAGACCCCCGTGCTCAGCCTGCTGCGGGCGGG
 AGGCGCGCGCGCCCTCGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG
 AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCCTGGGAAGACGTCGGCCTGGCCC
 TGTGCCGCACTCAGGACCCCGCGGGCCTGGTGGCCCTCTGGACAAGCCGGGGCTGGCCGGCCCCCAC
 AGCTGGTCTTGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGCACGCCTGGCCCCGA
 TGGCGGGCCAGTGGGGGGTGAAGCACCGGTACCCCGGGCGGTCTCCTCGGCTGTGACATCGCCC
 GTGCCCCGTGGGGTGTGGAGGCCGTACCTCCCGGCCCCCACTGGCTGTTGGGGACACCACTGCCGCC
 CAAGGCCCTGCCACCCGCGGGGTGCCACAGGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCC
 GCTGGAGGCCGCCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGGCACTGCGGCCAGGT
 GCAGCCGAAGCGAGCCCTCCTCCCCGCCCCGGTCAACTGCGGGGACCTGCAGCCGCGCGGGCCCCGA
 GTCCCCGGGGCGCTTCTTGGCACGGTTCTTGGCCAACACGTCTTCCAGGGCCGCAACGGGCCCGGTG
 TGGGTGACAGGCAGCTCCCCAGACGAAGACGGGCAGTGCCAGCGGGGAGCTGTGCCTGGACCCT
 GGCACCAACGACTCGGCCACCCCTGGACGCACTGTTCCCGCGCTGGCCAACGGCTCAGCGCCCCGT
 GCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCC
 TTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACC
 GGCCTGGTGGGGACCTGCTGGCCGGCCGGGGCCACATGGCGGTCAACAGCTTCAGTATCAACTCC
 GCCCCGTCAAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGGG
 CACGGGACACGGCCCTCACCATCGGTGCCTTTATGTGGCCCTGCACTGGTCCACGTGGCTGGGCGT
 CTTTGGCGCCCTGCACTCAACGCGCTCTTCTCAACGTGTACGAGTGGCGTAGCCCCCTACGGCCCTC
 ACGCCACGTGGCGCGCAACCGCAGCACCGTCTTCTCTCACTCTCAGCCCTCAACCTGTGCTACGCCA
 TCCTCTTCAGACGCAACCGTGTCCAGCAAGCCCAAGTGCCCCACGGGCCCGCTGCTCATGAACCT
 CTGGGCCATCTTCTGCTGTGTGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTATGGTGGGG
 GACAAGACCTTCGAGGAGCTGTGGGGATCCACGACCCCAAGGGCTTCCGCTTCGGCACCGTGTGG
 GAGAGCAGCGCCGAGGCGTACATCAAGAAGAGCTTCCCCGACATGCACGCACACATGCGGCGCCAC
 AGCGCGCCACCAACGCCCCGCGGCGTGCCTATGCTCACGAGCGACCCCCCAAGCTCAACGCCCTTC
 ATCATGGACAAGTCGCTCCTGGACTACGAGGTCTCCATCGACGCGGACTGCAAACCTGCTGACCGTGG
 GAAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCCAGAACTCGCCGCTCACCTCCAACCT
 GTCCGAGTTCATCAGCCGCTACAAGTCTTCCGGCTTCATCGACCTGCTCCACGACAAGTGGTACAAG
 ATGGTGCCTTGGCGCAAGCGGGTCTTGGCGTTACAGAGACCCTGCAGATGAGCATCTACCACITCG
 CGGGCCTCTTCGTGTTGCTGTGCCTGGGCCTGGGCAGCGCTCTGCTCAGCTCGCTGGGGGAGCACGC
 CTTCTTCCGCTGGCGCTGCCGCGCATCCGCAAGGGGAGCAGGCTGCAGTACTGGCTGCACACCAGC
 CAGAAAATCCACCGCGCCCTCAACACGGAGCCACCAGAGGGGTGGAAGGAGGAGACGGCAGAGGC
 GGAGCCCAGCGGCCCCGAGGTGGAGCAGCAGCAGCAGCAGGACCAGCCAACGGCTCCGGAGG
 GCTGGAAACGGGCGCGCCGGGCGGTGGACAAGGAGCGCCGCGTGGCTTCTGCTGGAGCCCCCGG
 TGTTTGTGGACCCGAAGCGGACGCGGAGGCGGAGGCTGCGCCGCGAGAGGGCCCCGTCTGGCTGT
 GCTCCTACGGCCGCCCGCCCGCCGCAAGGCCACGGGGGCCCCCCAGCCCGGGGAGCTGCAGGAGC
 TGGAGCGCCGCATCGAAGTCGCGCGTGAGCGGCTCCGCCAGGCCCTGGTGGCGCGCGGCCAGCTCC
 TGGCACAGCTCGGGGACAGCGCACGTACCGGCCTCGGCGCTTGCTTCAGGCCAGAGCGGCCCCCCG
 CGGAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 8

MEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVLISLLRREARAP
LGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTLQDPGGLVALWTSRAGRPPQLVLDLS
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTFLPPKALFTAGLP
PGLLALGEVARPPLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCGLQAGPESPGRFLARFLANT
SFQGRTPGVWVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
LAEDTPFDLFLYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFFSTSLGI
MVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFTVYEWRSPLYGLTPRGRNRSTVFSYSSALNLC
YAILFRRTVSSKTPKCPGTGRLLMNLWAFCLLVLSYTANLAAMVVGDKTFEELSGIHDPKGFRFGTVWE
SSAEAYIKKSFPDMHAHMRRHSAPTTFRGVAMLTSDPPKLNAFIMDKSLDYEVSIDADCKLLTVGKPF
AIEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFAVTETLQMSIYHFAGLFVLLC
LGLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAEPSGPEVEQQQQ
QQDQPTAPEGWKRARRAVDKERRVRFLLEPAVVVAPEADAEAEAAPREGPVWLCSYGRPPAARPTGAP
QPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSGRPGSQE

FIG. 9

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(5) = 0.0

Identities = 928/1076 (86%), Positives = 928/1076 (86%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGCGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G
Sbjct: 22736 CCCTGCC-CCTAGGTTCCTGGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCCGTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGCGGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCCG 960
CC GG C C GGG G C G CC GG CA C G G AGC C C GCC G
Sbjct: 22850 CCGGGACCCACGGGGCGCCCCGGCCTGGGCCA-CGGTGGGCAGCTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCCGAGTCCCCGGGGCG-CTTCTTGGCAGC 1019
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTGCCTCTGCAGC-GCCCCCGCCCCACAGGGTGGCCAG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCTTCCAGGGCCCGCACGGGC-CCCCTGTGGGTGACAGGCA 1075
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C
Sbjct: 22965 GT--CTGGCCCAAGCTGCGTG-TGTAACGCTGTTGGAACACCCATTTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAGTGCCAGCGGGGCAGCTGTGCCTGGACCCCTGGCACCA 1135
G CCAGACGAAGACGGGCAGTGCCAGCGGGGCAGCTGTGCCTGGACCCCTGGCACCA
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTGCCAGCGGGGCAGCTGTGCCTGGACCCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCCCTGGACGCACTGTTTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 1195
ACGACTCGGCCACCCCTGGACGCACTGTTTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG
Sbjct: 23080 ACGACTCGGCCACCCCTGGACGCACTGTTTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255
CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA
Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 1315
CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG
Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 23259

Query: 1316 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 1375
GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA
Sbjct: 23260 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 1435
GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA
Sbjct: 23320 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGCGGGACGGGACACGGCCTCACCATCGGTGCCTTTATGT 1495
CCAGCCTGGGCATCATGGTGCGGGACGGGACACGGCCTCACCATCGGTGCCTTTATGT
Sbjct: 23380 CCAGCCTGGGCATCATGGTGCGGGACGGGACACGGCCTCACCATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT 1555
GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCT

FIG. 9 Continued

Sbjct: 23440 GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTTGGCGCCCTGCACCTACCGCGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 1615
TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA

Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 1675
GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA

Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGGCA 1735
CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGGCA

Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGGCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGTCTCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG 1795
TCTTCTGCCTGCTGGTGTCTCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG

Sbjct: 23680 TCTTCTGCCTGCTGGTGTCTCAGCTACACGGCCAACCTGGCTGCCGTATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGGCTTCCGCTTCGGCACCG 1855
ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGG C GC TCGG

Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGTGGCGGGCTCGGGGGGC 23799

Query: 1856 TGTGGGAG 1863
TG GGG G

Sbjct: 23800 TGGGGGTG 23807

FIG. 10

Score = 2426 (854.0 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 463/474 (97%), Positives = 464/474 (97%), Frame = +1

Query: 1063 WVTGSSPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
+V PDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct: 427 FVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPDFDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
LAEDTPDFDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTPDFDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEYWRSPYGLTPR 1602
PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEYWRSPYGLTPR
Sbjct: 547 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEYWRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAIFFCLLVLSSTANLAA 1782
GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAIFFCLLVLSSTANLAA
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAIFFCLLVLSSTANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPK-----GFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 1944
VMVGDKTFEELSGIHDPK GFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 726

Query: 1945 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 2124
RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN
Sbjct: 727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 786

Query: 2125 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2304
LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2305 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 2466
LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 900

FIG. 11

Gltamate_Receptor_RAT_AAD4165 MRRSLWVLLSRCLLLPPPCALVLAGVPSSSSHPPQPCQLKRECHAVRGAHLPQWTT
Gltamate_Receptor_Human_06039 MEFVRALWLG--LALALGP-----GS--AGGHPQPCCGLARLGGSVRLGALLPR--
21659259_EXT MEFVRALWLG--LALALGP-----GS--AGGHPQPCCGLARLGGSVRLGALLPR--

Gltamate_Receptor_RAT_AAD4165 APRAASRAQEGGRRAAQEDDPESGTWRPPAPSSQARWLGSAIHGEGPPGSRKLGEAGAGAE
Gltamate_Receptor_Human_06039 APLARARA---RAALAR---AALAPF---
21659259_EXT APLARARA---RAALAR---AALAPF---

Gltamate_Receptor_RAT_AAD4165 TLWPRDALLFAVENLNRVEGLLPYNLSLELVMAIEAGLGDLPLMPFSSPSSPWSSDFEFSE
Gltamate_Receptor_Human_06039 LPHNLSLELVVAAPP-----ARDPASL
21659259_EXT LPHNLSLELVVAAPP-----ARDPASL

Gltamate_Receptor_RAT_AAD4165 LOSCHTUVVOGVSAALLAFPOSQGEHLDLSSSVLHIVLSREFF--PRESQNLHL
Gltamate_Receptor_Human_06039 TRGLCQALVPPGVAAALLAFPEARPELLQLHFLAAATETPVL SLLRREARAPLGAPNPFHL
21659259_EXT TRGLCQALVPPGVAAALLAFPEARPELLQLHFLAAATETPVL SLLRREARAPLGAPNPFHL

Gltamate_Receptor_RAT_AAD4165 QLSLENSLSADADWTVSILTMNNYNFSLLLCQEDWNI TDFLL TENNSKFHLESVIN
Gltamate_Receptor_Human_06039 QLHWASPLETLLDVLVAVLQAHAWEDVGLAL CRTQDPGGI VALWTSRAG--RPPQLVLDLS
21659259_EXT QLHWASPLETLLDVLVAVLQAHAWEDVGLAL CRTQDPGGI VALWTSRAG--RPPQLVLDLS

Gltamate_Receptor_RAT_AAD4165 ANLSTIKDLSFLQVQMDNR--NSTPTMVFQCDSDSIQGFEMSTQFG--SPPELHWL
Gltamate_Receptor_Human_06039 RRD TGDAGLFLARLAPMAAPVGG EAPVPAAVLLGCDIARARRVLEA-----PPGPHWLL
21659259_EXT RRD TGDAGLFLARLAPMAAPVGG EAPVPAAVLLGCDIARARRVLEA-----VPPGPHWLL

Gltamate_Receptor_RAT_AAD4165 GDSQNVEEELRTGLPLGLAHKTIQSVFYYQDAELVARAATATMQLLELALIPST
Gltamate_Receptor_Human_06039 GTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHDI VQLVARALGSAAQVQPKRALLPAP
21659259_EXT GTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHDI VQLVARALGSAAQVQPKRALLPAP

Gltamate_Receptor_RAT_AAD4165 VNCMDKKTIN-LSSQLSRFLANTFRGLGSGKVKGSIISSSENNFFVNLQHDPMK
Gltamate_Receptor_Human_06039 VNCGLDLPAGFESPGRFLARFLANTSFQGRTPGVWVTGSSQHMSRHEKWSLRRDRKA
21659259_EXT VNCGLDLPAGFESPGRFLARFLANTSFQGRTPGVWVTGSSQHMSRHEKWSLRRDRKA

Gltamate_Receptor_RAT_AAD4165 PMWTRGCSWQGRIVVSGIWP EQAQKHKTHFQHPNKLHVRVTL EHPFVETREVDG
Gltamate_Receptor_Human_06039 PAWATIGSWRDSQDPE--GASARPPPPQGAQVWP KLRVTL EHPFVETREVDG
21659259_EXT PAWATIGSWRDSQDPE--GASARPPPPQGAQVWP KLRVTL EHPFVETREVDG

Gltamate_Receptor_RAT_AAD4165 LCPAGQLCLDPMTNDSSMLDRFLPSLHSSNDVPIKFKECCYGYCIDLLEQLAEDMNFDF
Gltamate_Receptor_Human_06039 QCPAGQLCLDPMTNDSSATLDALFAALANG--SAPRALRECCYGYCIDLLEQLAEDTPDFD
21659259_EXT QCPAGQLCLDPMTNDSSATLDALFAALANG--SAPRALRECCYGYCIDLLEQLAEDTPDFD

Gltamate_Receptor_RAT_AAD4165 DLYLVGDGKYGAWNGHWTGLVGDLLSTIANMAVT SFSINARSQVDFTSPPFFSTSLGI
Gltamate_Receptor_Human_06039 ELYLVDGKYGALRDGRWTGLVGDLLAGRAHMAVT SFSINARSQVDFTSPPFFSTSLGI
21659259_EXT ELYLVDGKYGALRDGRWTGLVGDLLAGRAHMAVT SFSINARSQVDFTSPPFFSTSLGI

Gltamate_Receptor_RAT_AAD4165 EVRTDRTAAPIGAFMWPLHWSWLVGLFVALHHTAFELTVEWESPQCTPFGGRNRSVFS
Gltamate_Receptor_Human_06039 MVRAEDTASPIGAFMWPLHWSWLVGLFVALHHTAFELTVEWESPQCTPFGGRNRSVFS
21659259_EXT MVRAEDTASPIGAFMWPLHWSWLVGLFVALHHTAFELTVEWESPQCTPFGGRNRSVFS

Gltamate_Receptor_RAT_AAD4165 YSSALNLCYAILFGRTAAIKPPEKWTGFLMLNLWAI FCLLVLSY TANLA AVMVGDKTFE
Gltamate_Receptor_Human_06039 YSSALNLCYAILFRRTVSSKTPKCPTRLLMLNLWAI FCLLVLSY TANLA AVMVGDKTFE
21659259_EXT YSSALNLCYAILFRRTVSSKTPKCPTRLLMLNLWAI FCLLVLSY TANLA AVMVGDKTFE

Gltamate_Receptor_RAT_AAD4165 ELSGIHD PKLHHPSSQGRFGTVRES SAEDYQSFPMHEYMRRYVNPATPDGVQYKND
Gltamate_Receptor_Human_06039 ELSGIHD PKLHHPAGGFRFGTVWESSAEAYIKESFDDMHAMRRHSAPTPRGVAMLTSD
21659259_EXT ELSGIHD PK-----GFRFGTVWESSAEAYIKESFDDMHAMRRHSAPTPRGVAMLTSD

Gltamate_Receptor_RAT_AAD4165 PEKLDALIMDHALLDYEVSIDADCKLLTVGKPPAIEGYGIGLPPNSPLTSHSELISQWK
Gltamate_Receptor_Human_06039 PPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPPNSPLTSHSELISRYK
21659259_EXT PPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPPNSPLTSHSELISRYK

Gltamate_Receptor_RAT_AAD4165 SHGFMDLHDKWYVVPCKGRSFAVTETLQMGIKHFSGLFVLLCGLSGLGEHIV
Gltamate_Receptor_Human_06039 SSGFIDLHDKWYVVPCKGRVFAVTETLQMSIYHFAGLFVLLCGLSGLGEHAF
21659259_EXT SSGFIDLHDKWYVVPCKGRVFAVTETLQMSIYHFAGLFVLLCGLSGLGEHAF

Gltamate_Receptor_RAT_AAD4165 HRLLLPRIKNSQLQYWLHTSQFHRAALNTSFVEEKQPSEKTKRVERRWRWTKTEGD
Gltamate_Receptor_Human_06039 FRLALPRIKGRSLQYWLHTSQKIHRALNTEPPEGSS--KEETAEAEPF-----GP--
21659259_EXT FRLALPRIKGRSLQYWLHTSQKIHRALNTEPPEGSS--KEETAEAEPF-----GP--

Gltamate_Receptor_RAT_AAD4165 SEISLFPSSNLGPQQLMVNTSNLSHNDNQRYIFND EEQNQLGTQAHQD IPLQRREL
Gltamate_Receptor_Human_06039 -EEEQQQQQQDQPTAPEGWKRARRAVKEERVRFLLEPQVVVAPEADAEA EAAE--REG
21659259_EXT -EEEQQQQQQDQPTAPEGWKRARRAVKEERVRFLLEPQVVVAPEADAEA EAAE--REG

Gltamate_Receptor_RAT_AAD4165 PASLTINPADSLNVTSSV IQELS ELEKQIQWIRQELQLASRE-TELEYQKINETCE
Gltamate_Receptor_Human_06039 PVWLCYGRPPAARP TGAPQPGELQELERTEARERERLQATVREGQLAQIGDAAHRP
21659259_EXT PVWLCYGRPPAARP TGAPQPGELQELERTEARERERLQATVREGQLAQIGDAAHRP

Gltamate_Receptor_RAT_AAD4165 S-----
Gltamate_Receptor_Human_06039 -----
21659259_EXT RRL LQARAAPAEAPPHSGRPGSQE

FIG. 12

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCTGGCGCTGGCGCTGGGGCCGGGGTCCGCGGGGGGC
 CACCCTCAGCCGTGCGGCGTCTTGGCGCGCTCGGGGGCTCCGTGCGCCTGGGCGCCCTCCTGCCCC
 GCGCGCCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCGCGCCTGGCGCCGCGGCTGCC
 GCACAACTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCGCGACCCCGCCTCGCTGACCCGC
 GGCCTGTGCCAGGCGCTGGTGCCTCCGGGCGTGGCGGCCCTGCTCGCCTTTCCCGAGGCTCGGCCCG
 AGCTGCTGCAGCTGCACCTTCTGGCGGCGGCCACCGAGACCCCGTGTCTCAGCCTGCTGCGGCGGG
 AGGCGCGCGCGCCCTCGGAGCCCCGAACCCATTCCACCTGCAGCTGCACCTGGGCCAGCCCCCTGG
 AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGACGTGGGCTGGCCC
 TGTGCCCACTCAGGACCCCGCGCGCCTGGTGGCCCTCTGGACAAGCCGGGCTGGCCGGCCCCCAC
 AGCTGGTCTTGGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGCACGCTGGCCCCGA
 TGGCGGCGCCAGTGGGGGGTGAAGCACCGGTACCCGCGCGGCTCCTCCTCGGCTGTGACATCGCCC
 GTGCCCGTCCGGTGTGGAGGCGGTACCTCCCGGCCCCCACTGGCTGTTGGGGACACCACTGCCGCC
 CAAGGCCCTGCCACCCGCGGGGCTGCCACCGGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCC
 GCTGGAGGCCCGCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGGCAGTGCGGCCAGGT
 GCAGCCGAAGCGAGCCCTCCTCCCGCCCCCGGTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCCGA
 GTCCCCGGGGCGCTTCTTGGCACGGTTCCTGGCCAACACGTCTTCCAGGGCCGACCGGGCCCCGTG
 TGGGTGACAGGACGCTCCCAAGACGAAGACGGGCACTGCCAGCGGGGACGCTGTGCTTGGACCTT
 GGCACCAACGACTCGGCCACCTTGGACGCACTGTTCCGCGCGCTGCCAAACGGCTCAGCGCCCCGT
 GCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCC
 TTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACCGCCGCTGGACC
 GGCCTGGTCCGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCAACAGCTTCAGTATCAACTCC
 GCCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCACAGCCTGGGCATCATGGTGGGG
 CACGGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCCCTGCACTGGTCCACGTGGCTGGGCGT
 CTTTGGCGCCCTGCACCTCACCGCGCTCTTCTCACCCTGTACGAGTGGCCTAGCCCCCTACGGCCTC
 ACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCA
 TCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGCGCCTGCTCATGAACCT
 CTGGGCCATCTTCTGCCTGCTGGTGTGTCCAGCTACACGGCCAACCTGGCTGCCGTGCTGGTGGG
 GACAAGACCTTCGAGGAGCTGTGCGGGATCCAAGACCCCAAGCTGCACACCCGGGCGCAGGGCTT
 CCGCTTCGGCACCGTGTGGGAGAGCAGCGCCGAGGCGTACATCAAGAAGAGCTTCCCCGACATGCA
 CGCACACATGCGGCGCCACAGCGCGCCACACGCCCCGCGGCGTCCGCTATGCTCACGAGCGACCC
 CCCCAGCTCAACGCCCTTCATCATGGACAAGTCGCTCCTGGACTACGAGGTCTCCATCGACGCCGAC
 TGAAACTGCTGACCGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCCAGAAC
 TCGCCGCTCACCTCCAACCTGTCCGAGTTCATCAGCCGCTACAAGTCTCCGGCTTCATCGACCTGT
 CCACGACAAGTGGTACAAGATGGTGCCTTGGCGCAAGCGGGTCTTTGCGGTTACAGAGACCTGCA
 GATGAGCATCTACCACTTCGCGGGCCTCTTCGTGTTGCTGTGCCTGGGCCCTGGGCAGCGCTCTGCTC
 AGCTCGCTGGGCGAGCACGCTTCTTCCGCTGGCGCTGCCGCGCATCCGCAAGGGGAGCAGGCTG
 CAGTACTGGCTGCACACCAGCCAGAAAATCCACCGCGCCCTCAACACGGAGCCACAGAGGGGTGCG
 AAGGAGGAGACGGCAGAGGCGGAGCCAGCGGCCCCGAGGTGGAGCAGCAGCAGCAGCAGCAGG
 ACCAGCCAACGGCTCCGAGGGCTGGAAACGGGCGCGCCGGGCGGTGGACAAGGAGCGCGCGGTG
 CGCTTCTGCTGGAGCCCCCGCGTGGTGTGGCACCCGAAGCGGACCGCGGAGGCGGAGGCTGCGCCG
 CGAGAGGGCCCCGTCTGGCTGTGCTCCTACGGCCGCCCCCGCCGCGCAAGGCCACGGGGGGCCCCC
 CAGCCCCGGGAGCTGCAGGAGCTGGAGCGCCGATCGAAGTCGCGCGTGAAGCGCTCCGCCAGGCC
 CTGGTGGCGCGCGGCCAGCTCCTGGCACAGCTCGGGGACAGCGCACGTACCCGCCCTCGGCGCTTG
 CTTAGGCCAGAGCGGCCCCCGCGGAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 14

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(3) = 0.0
Identities = 948/1107 (85%), Positives = 948/1107 (85%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G
Sbjct: 22736 CCCTGCC-CCTAGGTTCTTGGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCCGTGTG 22792

Query: 848 AGGTGGCAG-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCCG 960
CC GG C C GGG G C G CC GG CA C G G AGC C C GCC G
Sbjct: 22850 CCGGGACCCACGGGGCGCCCCGGCCTGGGCCA-CGGTGGGCAGCTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCGAGTCCCCGGGGCG-CTTCTTGGCAG 1019
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTGCCCTCTGCACG-GCCCCCGCCCCACAGGGTGCCCG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCCTTCCAGGGCCGACGGGC-CCCGTGTGGGTGACAGGCA 1075
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C
Sbjct: 22965 GT--CTGGCCCAAGCTGCGTG-TGGTAACGCTGTTGGAACACCCATTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAGTGGCCAGCGGGGACCTGTGCCTGGACCCCTGGCACCA 1135
G CCAGACGAAGACGGGCAGTGGCCAGCGGGGACCTGTGCCTGGACCCCTGGCACCA
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTGGCCAGCGGGGACCTGTGCCTGGACCCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCCTGGACGCACGTGTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 1195
ACGACTCGGCCACCCTGGACGCACGTGTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG
Sbjct: 23080 ACGACTCGGCCACCCTGGACGCACGTGTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

FIG. 14 Continued

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255
 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA
 Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGGACG 1315
 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGGACG
 Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGGACG 23259

Query: 1316 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCACCA 1375
 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCACCA
 Sbjct: 23260 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 1435
 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA
 Sbjct: 23320 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGCGGGGACGGGACACGGCCTCACCCTATCGGTGCCTTTATGT 1495
 CCAGCCTGGGCATCATGGTGCGGGGACGGGACACGGCCTCACCCTATCGGTGCCTTTATGT
 Sbjct: 23380 CCAGCCTGGGCATCATGGTGCGGGGACGGGACACGGCCTCACCCTATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCCTGCACTGGTCCACGTGGCTGGGGCTCTTTGCGGGCCCTGCACCTCACC CGGCTCT 1555
 GGCCCCCTGCACTGGTCCACGTGGCTGGGGCTCTTTGCGGGCCCTGCACCTCACC CGGCTCT
 Sbjct: 23440 GGCCCCCTGCACTGGTCCACGTGGCTGGGGCTCTTTGCGGGCCCTGCACCTCACC CGGCTCT 23499

Query: 1556 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCAGGCCACGTGGCCGCAACCGCA 1615
 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCAGGCCACGTGGCCGCAACCGCA
 Sbjct: 23500 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCAGGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 1675
 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA
 Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 1735
 CCGTGTCCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA
 Sbjct: 23620 CCGTGTCCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG 1795
 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG
 Sbjct: 23680 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCCAAGCTGCACCACC-CGGCGCAG 1854
 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCCAAG TG C CC CGG G G
 Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCCAAGGTGGGCGGCCTCGG-G--G 23796

Query: 1855 GGCTTCCGCTTCGGGCACCGTGTGGGAGAGCAGCG-CCGAGG 1894
 GGCT C G T GGC G G GGG AGC G G CC GG
 Sbjct: 23797 GGCTGCGGGT--GGCCTTGGG-GGGCTAGCGGTGGCCCCGG 23834

FIG. 15

Score = 2481 (873.4 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 469/474 (98%), Positives = 470/474 (99%), Frame = +1

Query: 1063 WVTGSSPDEDGQCPCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
+V PDEDGQCPCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct: 427 FVFARDPDEDGQCPCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPPDEFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
LAEDTPPDEFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTPPDEFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPR 1602
PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPR
Sbjct: 547 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA 1782
GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFPMHAHMRRHSAPTTP 1962
VMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFPMHAHMRRHSAPTTP
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFPMHAHMRRHSAPTTP 726

Query: 1963 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFIEGYGIGLPQNSPLTSN 2142
RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFIEGYGIGLPQNSPLTSN
Sbjct: 727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPFIEGYGIGLPQNSPLTSN 786

Query: 2143 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2322
LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVFAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRVFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2323 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 2484
LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 900

FIG. 16

Glutamate_Receptor_RAT_AAD4165 MRRSLWVLSRCLLPDPICALVLA GVPSSSSHPPQPCOLKFGHVRGAGHLQPWTT
Glutamate_Receptor_Human_06039 MEFVRLWLG--LALALGP-----GS--AGGHPQPCGVLARLGGSVRLGALLPR....
21659259_EXT2 MEFVRLWLG--LALALGP-----GS--AGGHPQPCGVLARLGGSVRLGALLPR....

Glutamate_Receptor_RAT_AAD4165 APRASRAQEGGRAGAQRDDPESGTWRPPAPSGGARWLGSALHGSGPPGSRKLGEGAGAE
Glutamate_Receptor_Human_06039 APLARARA--RAALAR-----AALAPR-----
21659259_EXT2 APLARARA--RAALAR-----AALAPR-----

Glutamate_Receptor_RAT_AAD4165 TLWPRDALLFAVENLNRVEGL LFPYNLSLELVMAIEAGLGDLPLMPFSSPS SPWSSDPFFSF
Glutamate_Receptor_Human_06039 -----LPHNLSLELVVAAPP-----ARDPASL
21659259_EXT2 -----LPHNLSLELVVAAPP-----ARDPASL

Glutamate_Receptor_RAT_AAD4165 LQSCHTIVQGVSAALLAFQPSQGEEMELDLSSSVLHIPVLSGRRHF--PRESQNPFLHL
Glutamate_Receptor_Human_06039 TRGLCQALVPPGVAAALLAFPEARPELLQLHFLAAATETPVL SLLREARAPLGAPNPFHL
21659259_EXT2 TRGLCQALVPPGVAAALLAFPEARPELLQLHFLAAATETPVL SLLREARAPLGAPNPFHL

Glutamate_Receptor_RAT_AAD4165 QLSLENSLSADADVIVSLITMNNWYNFSLLLCQEDWNITDFLLTENNASKFHLESVIN
Glutamate_Receptor_Human_06039 QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSRAG--RPPQLVLDLS
21659259_EXT2 QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSRAG--RPPQLVLDLS

Glutamate_Receptor_RAT_AAD4165 ANLSIKDLSLFLQVQMDNR--NSTPTIMVFCDDSDSIFQTEFMSTQFG--SPPELHWVL
Glutamate_Receptor_Human_06039 RRDGTGAGLRARLAPMAAPVGGGEAPVPAAVLLGCDIARARRVLEA-----PPGPHWLL
21659259_EXT2 RRDGTGAGLRARLAPMAAPVGGGEAPVPAAVLLGCDIARARRVLEA-----VPPGPHWLL

Glutamate_Receptor_RAT_AAD4165 GDSQNVEELETEGLPLGLAHKKTQSVFYYQDAELVARAATMQLPELALLPST
Glutamate_Receptor_Human_06039 GTPLPKALPTAGLPGLLALGEVARPPLEAAIHDIVQLVARALGSAQVQPKRALLPAP
21659259_EXT2 GTPLPKALPTAGLPGLLALGEVARPPLEAAIHDIVQLVARALGSAQVQPKRALLPAP

Glutamate_Receptor_RAT_AAD4165 MNCMDKKTINLSQQLSRFLANTFRGLSGSKVKGSHISSENFFVNLQHPDMCK
Glutamate_Receptor_Human_06039 VNCGLQPAGEPSPGRFLARFLANTSFQGRTPGVWVTGSSQHMSRHKFKVSLRRDPRFA
21659259_EXT2 VNCGLQPAGEPSPGRFLARFLANTSFQGRTPGVWVTGSS-----P....

Glutamate_Receptor_RAT_AAD4165 PMVTRIGSWQGRIVVSGIWP EQAQRHKTHFQHPNKLHVRVTL EHPFVFTEVDGEG
Glutamate_Receptor_Human_06039 PAWATIGSWRDGQD--PG--GASARPPPPQGAQVWPKLRVVTL EHPFVFTEVDGEG
21659259_EXT2 -----P-----DEDG-----DEDG

Glutamate_Receptor_RAT_AAD4165 LCPAGQLCLDPMTNDSSMLDRLESSLHSSNDVPKIFKCCYGYCIDLLEQLAEDMNFDF
Glutamate_Receptor_Human_06039 QCPAGQLCLDPTGTHDSATLDALFAALANG--SAPRALRCCYGYCIDLLERLAEDTPFDF
21659259_EXT2 QCPAGQLCLDPTGTHDSATLDALFAALANG--SAPRALRCCYGYCIDLLERLAEDTPFDF

Glutamate_Receptor_RAT_AAD4165 ELYVGDGKYGAWNGHWTLGVLGDLISGTANMAVTSFSINSARSQVDFTSPEFFSTSLGI
Glutamate_Receptor_Human_06039 ELYVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVDFTSPEFFSTSLGI
21659259_EXT2 ELYVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVDFTSPEFFSTSLGI

Glutamate_Receptor_RAT_AAD4165 MVRIRDTAAPIGAFMWPLHWLWLGFLVALHHTAFLTVIEWSPGCTTPGRNENKVS
Glutamate_Receptor_Human_06039 MVRARDTA SPIGAFMWPLHWSTWLG VFAALHTALFLTVIEWRSPVGLTPRGNRSTVFS
21659259_EXT2 MVRARDTA SPIGAFMWPLHWSTWLG VFAALHTALFLTVIEWRSPVGLTPRGNRSTVFS

Glutamate_Receptor_RAT_AAD4165 VSSALNLCYAILFGRTAAIEPPKCGWTGFLMNLWAI FCMFCLSYTANLA AAVVGDKTFE
Glutamate_Receptor_Human_06039 VSSALNLCYAILFRRTVSSKTPKCP TGRLLMNLWAI FCLLVLSY TANLA AAVVGDKTFE
21659259_EXT2 VSSALNLCYAILFRRTVSSKTPKCP TGRLLMNLWAI FCLLVLSY TANLA AAVVGDKTFE

Glutamate_Receptor_RAT_AAD4165 ELSGIHD PKLHHP SQGFRFGTVRESSAEDVRSFPMEHYMRRYNVPATPDGVQYLKND
Glutamate_Receptor_Human_06039 ELSGIHD PKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTT PRGVAMLTSD
21659259_EXT2 ELSGIHD PKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTT PRGVAMLTSD

Glutamate_Receptor_RAT_AAD4165 PEKLD AFIMDKALLDYEV SIDADCKLLTVGKPPAIEGYGIGLPNSPLTSNISELISQW
Glutamate_Receptor_Human_06039 PPKLNAFIMDKSLLDYEV SIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSNISEFISRYK
21659259_EXT2 PPKLNAFIMDKSLLDYEV SIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSNISEFISRYK

Glutamate_Receptor_RAT_AAD4165 SHGFIDLDHDKWYKVP CGKRSFAVTETLQMGKHFSGLFVLLCIGFLSGLGEGHIV
Glutamate_Receptor_Human_06039 SSGFIDLHDKWYKVP CGKRVFAVTETLQMSIYH FAGLFVLLCIGLGSALLSSLGEHAF
21659259_EXT2 SSGFIDLHDKWYKVP CGKRVFAVTETLQMSIYH FAGLFVLLCIGLGSALLSSLGEHAF

Glutamate_Receptor_RAT_AAD4165 HRLLPRIKNSLQYWLHTSQIHRALNTSFVEEKQPKSKTKRVEKSRWRRWTCKTEGD
Glutamate_Receptor_Human_06039 FRLALPRIKGSRLQYWLHTSQIHRALNTPEPES--KEETAEEAPR-----GP..
21659259_EXT2 FRLALPRIKGSRLQYWLHTSQIHRALNTPEPES--KEETAEEAPR-----GP..

Glutamate_Receptor_RAT_AAD4165 SEELSFPRSLGPPQLMVNTSNLSHDNQRYIENDEEQNQLGTQAHQDIPLEQRRREL
Glutamate_Receptor_Human_06039 -----EEQQQQQQDQPTAPEGVKRRARRAVDKERVRFLLEP VVVVAPEADAEAEAAE--REG
21659259_EXT2 -----EEQQQQQQDQPTAPEGVKRRARRAVDKERVRFLLEP VVVVAPEADAEAEAAE--REG

Glutamate_Receptor_RAT_AAD4165 PASLTINGLADS LNVTRSSVIQELSELSEQLQIQLQLASRR--TEEEYQKNQTC
Glutamate_Receptor_Human_06039 PVWLCSYGPAPPAARPFGAPQPGELQELERTEARERERLROAVEEGQLAQLGDSAEHRP
21659259_EXT2 -----

Glutamate_Receptor_RAT_AAD4165 S-----
Glutamate_Receptor_Human_06039 RRL LQARAAPAEAPPHSGRPGSQE
21659259_EXT2

FIG. 17

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCCTGGCGCTGGCGCTGGGGCCGGGGTCCGCGGGGGG
 CACCCTCAGCCGTGCGGCGTCTGGCGCGCTCGGGGGCTCCGTGCGCTGGGCGCCCTCCTGCCCC
 GCGCGCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCGCTGGCGCCGCGGCTGCC
 GCACAACCTGAGCTTGGAGCTGGTGGTCCGCGCGCCCCCGCCCGCGACCCCGCCTCGCTGACCCGC
 GGCCTGTGCCAGGCGCTGGTGCCTCCGGGCGTGGCGGCCCTGCTCGCCTTCCCGAGGCTCGGCCCC
 AGCTGCTGCAGCTGCACTTCTGGCGGCGGCCACCGAGACCCCGTGTCTCAGCCTGCTGCGGCGGG
 AGGCGCGCGGCCCTCGGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG
 AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGACGTGCGCCTGGCCC
 TGTGCCGCACTCAGGACCCCGCGGCGCTGGTGGCCCTCTGGACAAGCCGGGCTGGCCGGCCCCAC
 AGCTGGTCTGGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGGACGCTGGCCCCGA
 TGGCGGCGCCAGTGGGGGTGAAGCACCGGTACCCGCGGCGGTCTCTCGGCTGTGACATCGCCC
 GTGCCCCGTGCGGTGCTGGAGGCGGTACCTCCCGGCCCCCACTGGCTGTTGGGGACACCACTGCCGCC
 CAAGGCCCTGCCACCGCGGGGCTGCCACCAGGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCC
 GCTGGAGGCCGCCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGGCAGTGGCGCCAGGT
 GCAGCCGAAGCGAGCCCTCCTCCCCGCCCGGTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCGA
 GTCCCCGGGGCGCTTCTTGGCACGGTTCCTGGCCAACACGTCCTTCCAGGGCCGCACGGGCCCGTG
 TGGGTGACAGGCAGCTCCAGGTACACATGTCTCGGCACCTTAAGGTGTGGAGCCTTCGCCGGGACC
 CACGGGGCGCCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAACGGG
 GAGGTGCCTCTGCACGGCCCCCGCCCCACAGGGTGGCCAGGTCTGGCCCAAGCTGCGTGTGGTAA
 CGCTGTTGGAACACCCATTTGTGTTTGGCCGTGATCCAGACGAAGACGGGCAGTGCCAGCGGGGC
 AGCTGTGCCTGGACCTGGCACCAACGACTCGGCCACCTGGACGCACTGTTCCCGCGCTGGCCAA
 CGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTG
 GCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGG
 GACGGCCGCTGGACCGGCCTGGTGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCCAGC
 TTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTCTCCACCAGCCTGG
 GCATCATGGTGGGGGACGGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCACTGGTC
 CACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCTCCTCAGCCCTCA
 AGCCCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCCTCAGCCCTCA
 ACCTGTGCTACGCCATCCTCTTCAGACGCAACCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCG
 CCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCT
 GCCGTCATGGTGGGGGACAAGACCTTCGAGGAGCTGTGGGGGATCCACGACCCCAAGCTGCACCAC
 CCGGCGCAGGGCTTCCGCTTCGGCACCGTGTGGGAGAGCAGCGCCGAGGCGTACATCAAGAAGAGC
 TTCCCCGACATGCACGCACACATGCGGCGCCACAGCGCGCCACCAACGCCCGCGGGCGTCCCATG
 CTCACGAGCGACCCCCCAAGCTCAACGCCTTCATCATGGACAAGTCGCTCCTGGACTACGAGGTCT
 CCATCGACGCCGACTGCAAACTGCTGACCGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATCG
 GACTGCCCCAGAACTCGCCGCTCACCTCCAACCTGTCCGAGTTCATCAGCCGCTACAAAGTCTCCGG
 CTTATCGACCTGCTCCACGACAAGTGGTACAAGATGGTGCCTTGGCGCAAGCGGGTCTTTGCGGTT
 ACAGAGACCCTGCAGATGAGCATCTACCACTTCGCGGGCCTCTTCGTGTTGCTGTGCCTGGGCCTGG
 GCAGCGCTCTGCTCAGCTCGCTGGGCGAGCACGCCTTCTTCGGCCTGGCGCTGCCGCGCATCCGCA
 GGGGAGCAGGCTGCAGTACTGGCTGCACACCAGCCAGAAATCCACCGCGCCCTCAACACGGAGCC
 ACCAGAGGGGTGGAAGGAGGAGACGGCAGAGGCGGAGCCAGCGGCCCGGAGGTGGAGCAGCAGC
 AGCAGCAGCAGGACCAGCCAACGGCTCCGGAGGGCTGGAAACGGGGCGCGCCGGGGCGGTGGACAAG
 GAGCGCCGCGTGCCTTCTGCTGGAGCCCGCCGTGGTTGTGGCACCCGAAGCGGACGCGGAGGCG
 GAGGCTGCGCCGCGAGAGGGCCCCGTCTGGCTGTGCTCCTACGGCCGCCCGCCCGCCGCAAGGCC
 ACGGGGGCCCCCAGCCCGGGGAGCTGCAGGAGCTGGAGCGCCGATCGAAGTGGCGCGTGAGCG
 GCTCCGCCAGGCCCTGGTGGCGCGCGGCCAGCTCCTGGCACAGCTCGGGGACAGCGCACGTCACCG
 GCCTCGGCGCTGCTTCAGGCCAGAGCGGCCCGCCCGGAGGCCCCACCACACTCTGGCCGACCGGG
 GAGCCAGGAATGA

FIG. 18

MEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLAAATETPVLSLLRREARAP
LGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTCQDPGGLVALWTSRAGRPPQLVLDLS
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP
PGLLALGEVARPPLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCGLQAPGPESPGRFLARFLANT
SFQGRTPGVWVTGSSQVHMSRHFVWSLRDPRGAPAWATVGSWRDGLDLEPGGASARPPPPQGAQ
VWPKLRVVTLLHHPFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCI
DLLERLAEDTPFDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSSENSARSQVVDFTSPFFS
TSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYEWRSPLYGLTPRGRNRSTVFSYSSA
LNL CYAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSY TANLA AVMVGDKTFEELSGIHDPKLHHPA
QGFRFGTVWESSAEA YIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDAD
CKLLTVGKPFATIEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPVPCGKR VFAVTETLQMSIY
HFAGLFVLLCLGLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETA EAEP
SGPEVEQQQQQQDQPTAPEGWKRRARRAVDKERRVRFLEPAVVVAPEADAEAEAAPREGPVWLCSYG
RPPAARPTGAPQPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSG
RPGSQE

FIG. 19

Score = 5188 (778.4 bits), Expect = 0.0, Sum P(4) = 0.0

Identities = 1068/1092 (97%), Positives = 1068/1092 (97%), Strand = Plus / Plus

Query: 1019 GGTTCCTGGCCAACACGTCCTTCCAGGGCCGACGGGCCCCGTGTGGGTGACAGGCAGCT 1078
GGTTCCTGGCCAACACGTCCTTCCAGGGCCGACGGGCCCCGTGTGGGTGACAGGCAGCT

Sbjct: 22747 GGTTCCTGGCCAACACGTCCTTCCAGGGCCGACGGGCCCCGTGTGGGTGACAGGCAGCT 22806

Query: 1079 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG 1138
CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG

Sbjct: 22807 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG 22866

Query: 1139 CCCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACGGGGAG 1198
CCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACGGGGAG

Sbjct: 22867 CCCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACGGGGAG 22926

Query: 1199 GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCGTGTGG 1258
GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCGTGTGG

Sbjct: 22927 GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCGTGTGG 22986

Query: 1259 TAACGCTGTGTGGAACACCCATTTGTGTTTGGCCGTGATCCAGACGAAGACGGGCAGTGCC 1318
TAACGCTGTGTGGAACACCCATTTGTGTTTGGCCGTGATCCAGACGAAGACGGGCAGTGCC

Sbjct: 22987 TAACGCTGTGTGGAACACCCATTTGTGTTTGGCCGTGATCCAGACGAAGACGGGCAGTGCC 23046

Query: 1319 CAGCGGGGCAGCTGTGCCTGGACCCTGGCACCAACGACTCGGCCACCCCTGGACGCACTGT 1378
CAGCGGGGCAGCTGTGCCTGGACCCTGGCACCAACGACTCGGCCACCCCTGGACGCACTGT

Sbjct: 23047 CAGCGGGGCAGCTGTGCCTGGACCCTGGCACCAACGACTCGGCCACCCCTGGACGCACTGT 23106

Query: 1379 TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT 1438
TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT

Sbjct: 23107 TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT 23166

FIG. 19 Continued

Query: 1439 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 1498
 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG
 Sbjct: 23167 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 23226

Query: 1499 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCCCTGGTCGGGGACC 1558
 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCCCTGGTCGGGGACC
 Sbjct: 23227 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCCCTGGTCGGGGACC 23286

Query: 1559 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 1618
 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC
 Sbjct: 23287 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 23346

Query: 1619 AGGTGGTGGACTTCACAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGCGGCAC 1678
 AGGTGGTGGACTTCACAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGCGGCAC
 Sbjct: 23347 AGGTGGTGGACTTCACAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGCGGCAC 23406

Query: 1679 GGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCCCTGCACCTGGTCCACGTGGCTGG 1738
 GGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCCCTGCACCTGGTCCACGTGGCTGG
 Sbjct: 23407 GGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCCCTGCACCTGGTCCACGTGGCTGG 23466

Query: 1739 GCGTCTTTTGGCGCCCTGCACCTCACCGCGCTCTTCCTCACCGGTGTACGAGTGGCGTAGCC 1798
 GCGTCTTTTGGCGCCCTGCACCTCACCGCGCTCTTCCTCACCGGTGTACGAGTGGCGTAGCC
 Sbjct: 23467 GCGTCTTTTGGCGCCCTGCACCTCACCGCGCTCTTCCTCACCGGTGTACGAGTGGCGTAGCC 23526

Query: 1799 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCC 1858
 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCC
 Sbjct: 23527 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCC 23586

Query: 1859 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 1918
 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC
 Sbjct: 23587 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 23646

Query: 1919 CCACGGGCCGCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCT 1978
 CCACGGGCCGCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCT
 Sbjct: 23647 CCACGGGCCGCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCT 23706

Query: 1979 ACACGGCCAACCTGGCTGCCGTATGGTCGGGGACAAGACCTTCGAGGAGCTGTCCGGGA 2038
 ACACGGCCAACCTGGCTGCCGTATGGTCGGGGACAAGACCTTCGAGGAGCTGTCCGGGA
 Sbjct: 23707 ACACGGCCAACCTGGCTGCCGTATGGTCGGGGACAAGACCTTCGAGGAGCTGTCCGGGA 23766

Query: 2039 TCCACGACCCCAAGCTGCACCACC-CGGCGCAGGGCTTCCGCTTCGGCACCCTGTGGGAG 2097
 TCCACGACCCCAAG TG C CC CGG G GGGCT C G T GGC G G GGG
 Sbjct: 23767 TCCACGACCCCAAGGTGGGCGGCTCGG-G--GGGCTGCGGGT--GGCCTTGGG-GGGCT 23820

Query: 2098 AGCAGCG-CCGAGG 2110
 AGC G G CC GG
 Sbjct: 23821 AGCGGTGGCCCCGG 23834

FIG. 20

Score = 4730 (1665.0 bits), Expect = 0.0, P = 0.0

Identities = 900/900 (100%), Positives = 900/900 (100%), Frame = +1

Query: 1 MEFVRALWLGLALALPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARA 180
MEFVRALWLGLALALPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARA
Sbjct: 1 MEFVRALWLGLALALPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARA 60

Query: 181 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLA 360
ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLA
Sbjct: 61 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLA 120

Query: 361 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 540
AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR
Sbjct: 121 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 180

Query: 541 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 720
TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC
Sbjct: 181 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 240

Query: 721 DIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHNDIVQLV 900
DIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHNDIVQLV
Sbjct: 241 DIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHNDIVQLV 300

Query: 901 ARALGSAAQVQPKRALLPAPVNCGLDLPAGPESPGRFLARFLANTSFOGRTGPVWVTGSS 1080
ARALGSAAQVQPKRALLPAPVNCGLDLPAGPESPGRFLARFLANTSFOGRTGPVWVTGSS
Sbjct: 301 ARALGSAAQVQPKRALLPAPVNCGLDLPAGPESPGRFLARFLANTSFOGRTGPVWVTGSS 360

Query: 1081 QVHMSRHFVWVSLRRDPRGAPAWATVGSWRDGLDLEPGGASARPPPPQGAQVWPCLRVRV 1260
QVHMSRHFVWVSLRRDPRGAPAWATVGSWRDGLDLEPGGASARPPPPQGAQVWPCLRVRV
Sbjct: 361 QVHMSRHFVWVSLRRDPRGAPAWATVGSWRDGLDLEPGGASARPPPPQGAQVWPCLRVRV 420

Query: 1261 TLLEHPFVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 1440
TLLEHPFVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC
Sbjct: 421 TLLEHPFVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 480

Query: 1441 IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 1620
IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ
Sbjct: 481 IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 540

FIG. 20 Continued

Query: 1621 VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSP 1800
VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSP
Sbjct: 541 VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSP 600

Query: 1801 YGLTPRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 1980
YGLTPRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY
Sbjct: 601 YGLTPRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 660

Query: 1981 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAHMRRH 2160
TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAHMRRH
Sbjct: 661 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAHMRRH 720

Query: 2161 SAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQN 2340
SAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQN
Sbjct: 721 SAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQN 780

Query: 2341 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKR VFAVTETLQMSIYHFAGLFVLLCL 2520
SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKR VFAVTETLQMSIYHFAGLFVLLCL
Sbjct: 781 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKR VFAVTETLQMSIYHFAGLFVLLCL 840

Query: 2521 GLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAEF 2700
GLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAEF
Sbjct: 841 GLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAEF 900

FIG. 21

Glutamate_Receptor_RAT_AAD4165 MRRSLWVLSRCLLPFPCALVLAQVSSSSHPQPCQLKFGHAFVGGANHLQPWTT
 Glutamate_Receptor_Human_06039 MEFVRLWLG--LALALGP-----GS--AGCHPQPCGVLARLGGSVRLGALLPE----
 21659259_EXT3 MEFVRLWLG--LALALGP-----GS--AGCHPQPCGVLARLGGSVRLGALLPE----

Glutamate_Receptor_RAT_AAD4165 APRASRAQEGGRAGAQRDDPESGTWRPPAPSQGARWLGSLHGGPPGSRKLGEAGAE
 Glutamate_Receptor_Human_06039 APLARARA-----RAALAR-----AALAPR-----
 21659259_EXT3 APLARARA-----RAALAR-----AALAPR-----

Glutamate_Receptor_RAT_AAD4165 TLWPRDALLFAVENLNRVEGLLFYHLSLEWMAIEAGLGDLPLMPFSSPSPWSSDFEF
 Glutamate_Receptor_Human_06039 -----LPHNLSLELVVAAPP-----ARDPASL
 21659259_EXT3 -----LPHNLSLELVVAAPP-----ARDPASL

Glutamate_Receptor_RAT_AAD4165 LQSCHTGVQGVSAALLAFPPSQSGEMEDLDLSSSVLHIPVLSRRHF--PRESQNLHL
 Glutamate_Receptor_Human_06039 TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL SLLRREARAPLGAPNPFHL
 21659259_EXT3 TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL SLLRREARAPLGAPNPFHL

Glutamate_Receptor_RAT_AAD4165 QLSLENSLSADAVTVSLTMNNWYNFSLLCQEDWNIIDFLLTENNSKFHLESWIN
 Glutamate_Receptor_Human_06039 QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSRAG-RPPQLVLDLS
 21659259_EXT3 QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGGLVALWTSRAG-RPPQLVLDLS

Glutamate_Receptor_RAT_AAD4165 ANLSTKDLSFLQVQMDNRR--NSTPTMVMFGCDSDSIRQFEMSTQFGSPPELHWL
 Glutamate_Receptor_Human_06039 RRDTGDAGLRLARLAPMAAPVGGGEAPVPAAVLLGCDIARARRVLEA-----PPGPHWLL
 21659259_EXT3 RRDTGDAGLRLARLAPMAAPVGGGEAPVPAAVLLGCDIARARRVLEA-----VPPGPHWLL

Glutamate_Receptor_RAT_AAD4165 GDSQNVVELRTEGLPLGLAHGKTTQSVFYYQDAEELVARAVATMQLPELALLPST
 Glutamate_Receptor_Human_06039 GTPLPPKALPTAGLPGLLALGEVARPPLEAAIHDIVQLVARALGSAAQVQPKRALLPAP
 21659259_EXT3 GTPLPPKALPTAGLPGLLALGEVARPPLEAAIHDIVQLVARALGSAAQVQPKRALLPAP

Glutamate_Receptor_RAT_AAD4165 MNCMDPKTTN-LSSGQILSRFLANTFRGLSGSKVKSSISSENFFWNLQHDPMCK
 Glutamate_Receptor_Human_06039 VNCGLDLPAGPESPGRFLARFLANTSFQGRIGPVWVTGSSQVHMSRHFKWWSLRRDPGA
 21659259_EXT3 VNCGLDLPAGPESPGRFLARFLANTSFQGRIGPVWVTGSSQVHMSRHFKWWSLRRDPGA

Glutamate_Receptor_RAT_AAD4165 PMWTRGSGWQGRIVMSG IWP EQAQRHKTHFOHPNKLHLRVVTLLEHPFVFTFVVDG
 Glutamate_Receptor_Human_06039 PAWATVGSWFDGQLDLEPG---GASARPPPPQGAQVWPKL RVVTLLEHPFVFARDPDEDG
 21659259_EXT3 PAWATVGSWFDGQLDLEPG---GASARPPPPQGAQVWPKL RVVTLLEHPFVFARDPDEDG

Glutamate_Receptor_RAT_AAD4165 LCPAGQLCLDPMTNDSSMLDRLFS SLHSSNDVPIKFKCCYGYCIDLLEQLAEDMNFDF
 Glutamate_Receptor_Human_06039 QCPAGQLCLDPGTND SATLDALFAALANG--SAPRALRKCCYGYCIDLLERLAEDTPFDF
 21659259_EXT3 QCPAGQLCLDPGTND SATLDALFAALANG--SAPRALRKCCYGYCIDLLERLAEDTPFDF

Glutamate_Receptor_RAT_AAD4165 ELYVGDGKYGAWNGHWTGLVGDLLSTANMAVTSFINSARSQVDFTSPPFFSTSLGI
 Glutamate_Receptor_Human_06039 ELYLVGDGKYGALEDGRWTGLVGDLLAGRAHMAVTSFINSARSQVDFTSPPFFSTSLGI
 21659259_EXT3 ELYLVGDGKYGALEDGRWTGLVGDLLAGRAHMAVTSFINSARSQVDFTSPPFFSTSLGI

FIG. 22

| | | | |
|----------------|-----------------------|--------------|--|
| 21659259_EXT_3 | MEFVRALWGLLALGPGSAGGH | PQPCGV | LARLGGSVRLGALLPRAPLARARARAALARA |
| 21659259_EXT_2 | MEFVRALWGLLALGPGSAGGH | PQPCGV | LARLGGSVRLGALLPRAPLARARARAALARA |
| 21659259_EXT_1 | MEFVRALWGLLALGPGSAGGH | PQPCGV | LARLGGSVRLGALLPRAPLARARARAALARA |
| 21659259_EXT_3 | ALAPRLPHNLSLELVVAAP | PARDPAST | TRGLCQALVPPGVAALLAFPEARPELQLHFLA |
| 21659259_EXT_2 | ALAPRLPHNLSLELVVAAP | PARDPAST | TRGLCQALVPPGVAALLAFPEARPELQLHFLA |
| 21659259_EXT_1 | ALAPRLPHNLSLELVVAAP | PARDPAST | TRGLCQALVPPGVAALLAFPEARPELQLHFLA |
| 21659259_EXT_3 | AATEPVLSSLRREARAP | LGAPNPFHLQLH | WASPLETLIDVLVAVLQAHAWEDVGLALCR |
| 21659259_EXT_2 | AATEPVLSSLRREARAP | LGAPNPFHLQLH | WASPLETLIDVLVAVLQAHAWEDVGLALCR |
| 21659259_EXT_1 | AATEPVLSSLRREARAP | LGAPNPFHLQLH | WASPLETLIDVLVAVLQAHAWEDVGLALCR |
| 21659259_EXT_3 | TQDPGGLVALWTSRAGR | PQVLVLDLS | RRDTGDAGLKRARLAPMAAPVGGGEAPVPAAVLLGC |
| 21659259_EXT_2 | TQDPGGLVALWTSRAGR | PQVLVLDLS | RRDTGDAGLKRARLAPMAAPVGGGEAPVPAAVLLGC |
| 21659259_EXT_1 | TQDPGGLVALWTSRAGR | PQVLVLDLS | RRDTGDAGLKRARLAPMAAPVGGGEAPVPAAVLLGC |
| 21659259_EXT_3 | DIARARRVLEAVPPGP | HWLLGTPLP | PKALPTAGLPPGLLALGEVARPLEAAIHDIVOLV |
| 21659259_EXT_2 | DIARARRVLEAVPPGP | HWLLGTPLP | PKALPTAGLPPGLLALGEVARPLEAAIHDIVOLV |
| 21659259_EXT_1 | DIARARRVLEAVPPGP | HWLLGTPLP | PKALPTAGLPPGLLALGEVARPLEAAIHDIVOLV |
| 21659259_EXT_3 | ARALGSAAQVQPKRAL | LPAVNC | GDLQPAGPESPGRLARFLANTSFOGRTGPVWVTGSS |
| 21659259_EXT_2 | ARALGSAAQVQPKRAL | LPAVNC | GDLQPAGPESPGRLARFLANTSFOGRTGPVWVTGSS |
| 21659259_EXT_1 | ARALGSAAQVQPKRAL | LPAVNC | GDLQPAGPESPGRLARFLANTSFOGRTGPVWVTGSS |
| 21659259_EXT_3 | QVHMSRHF | KVWSLRDP | RGA PAWATVGSWRDQLDLEPGGASARPP PQGAQVWP |
| 21659259_EXT_2 | QVHMSRHF | KVWSLRDP | RGA PAWATVGSWRDQLDLEPGGASARPP PQGAQVWP |
| 21659259_EXT_1 | QVHMSRHF | KVWSLRDP | RGA PAWATVGSWRDQLDLEPGGASARPP PQGAQVWP |
| 21659259_EXT_3 | TLLEHPFVFARD | PDEBDGQCP | AGQLCLDPGTND SATLDALFAALANGSAPRALRKC |
| 21659259_EXT_2 | TLLEHPFVFARD | PDEBDGQCP | AGQLCLDPGTND SATLDALFAALANGSAPRALRKC |
| 21659259_EXT_1 | TLLEHPFVFARD | PDEBDGQCP | AGQLCLDPGTND SATLDALFAALANGSAPRALRKC |

FIG. 22 Continued

| | |
|----------------|-------------------------|
| 21659259_EXT_3 | RLLQARAAPAEAPPHSGRPGSQE |
| 21659259_EXT_2 | RLLQARAAPAEAPPHSGRPGSQE |
| 21659259_EXT_1 | RLLQARAAPAEAPPHSGRPGSQE |

FIG. 23

ACGCGTTACTCCTACCAGGTTGTAGCATGCATCTTTTTGAGAGAGCAGCTGGGATCGAGTA
TACTCTTGACTTAAATATGTTTGTATATAAAGACAAATGGAGAAATCAATTTTTTCCCTGA
ATTCTTAGGAGCACTTTAGTGAATAAAGAACCTGACAGTATGCTGGCCACATGTTTAAGG
ACAAAGGTGTCTGGGGAAATAAGCAAGATCATAGAGGAGCTTCTTAATTGACCGAAGTCC
TGAGTACTTCGAACCCATTTTGAACACTTGCCTCATGGACAGCTCATTGTAAATGATGGCA
TTAATTTATTGGGTGTGTTAGAAGAAGCAAGATTTTTTGGTATTGACTCATTGATTGAACAC
CTAGAAGTGGCAATAAAGAATTCTCAACCACCGGAGGATCATTACCAATATCCCGAAAGG
AATTTGTCCGATTTTTTGCTAGCAACTCCAACCAAGTCAGAACTGCGATGCCAGGGTTTGAA
CTTCAGTGGTGCTGATCTTCTCGTTTGGACCTTCGATACATTAACCTCAAAATGGCCAATT
TAAGCCGCTGTAATCTTGCACATGCAAATCTTTGCTGTGCAAATCTTGAACGAGCTGATCTC
TCTGGATCAGTGCTTGACTGTGCGAATCTCCAGGGAGTCAAGATGCTCTGTTCTAATGCAG
AAGGAGCATCCCTGAAACTGTGTAATTTTGAGGATCCTTCTGGTCTTAAAGCCAATTTAGA
AGGTGCTAATCTGAAAGGTGTGGATATGGAAGGAAGTCAGATGACAGGAATTAACCTGAG
AGTGGCTACCTTAAAAAATGCAAAGTTGAAGAACTGTAACTCAGAGGAGCAACTCTGGC
AGGAACTGATTTAGAGAATTGTGATCTGTCTGGGTGTGATCTTCAAGAAGCCAACCTGAGA
GGGTCCAACGTGAAGGGAGCTATATTTGAAGAGATGCTGACACCACTACACATGTCACAAA
GTGTCAGATGAGAATTTTAGGGGCTGGAGGAAGATGTAAAAGATGAAAATGTTTTCTTAT
CACTTTTCTTTCTCCACCCACTCAGTTGTCTAGAAGAAATAACACTGTAAGGAAATTTAAAA
AAAAAAA

FIG. 24

MLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLEEARFFGID
SLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGLNFSGADLSRLDLRYINFKMAN
LSRCNLAHANLCCANLERADLSGSVLD CANLQGVKMLCSNAEGASLKLCNFEDPSGLKANLE
GANLKGVDMEGSQMTGINLRVATLKN AKLKNCNLRGATLAGTDLENCDSLGC DLQEANLRGS
NVKG AIFEEMLTPLHMSQSVR

FIG. 25

Score = 1486 (523.1 bits), Expect = 1.4e-151, P = 1.4e-151

Identities = 286/286 (100%), Positives = 286/286 (100%), Frame = +1

Query: 130 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 309
RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI
Sbjct: 104 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 163

Query: 310 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL 489
NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL
Sbjct: 164 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL 223

Query: 490 NFSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGSVLDGANLQGVKMLCS 669
NFSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGSVLDGANLQGVKMLCS
Sbjct: 224 NFSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGSVLDGANLQGVKMLCS 283

Query: 670 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLKNCNLGA 849
NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLKNCNLGA
Sbjct: 284 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKNAKLKNCNLGA 343

Query: 850 TLAGTDLENCDSLGC DLQEANLRGSNVKGAI FEEMLTPLHMSQSVR 987
TLAGTDLENCDSLGC DLQEANLRGSNVKGAI FEEMLTPLHMSQSVR
Sbjct: 344 TLAGTDLENCDSLGC DLQEANLRGSNVKGAI FEEMLTPLHMSQSVR 389

FIG. 26

TTTCCAGGGTTCTAGCCTGTTTCATCTAGCCCC**ATG**ATGGCTGTGGACATCGAGTACAGATACAACCTGCAT
GGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACCAAAGCCCAGCAAACCACTGAGGCCT
TGTATTCAGCTGAGCAGCAAGAATGAAGCCAGTGAATGGTGGCCCCGGCTGTCCAGGAGAAGAAGGTGA
AAAAGCGGGTGTCTTTCGAGACAACCAGGGGCTGGCCCTGACAATGGTCAAAGTGTTCTCGGAATTCGA
TGACCCGCTAGATATGCCATTCAACATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAG
AGCGAGAGCTTTGTTCTGGATTTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGG
CCGACCACGTCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCACTGTGAAGGTTTCAGAA
CCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGCTACACAGACTTTCCT
TGTCAGTACGTGAAGGACACTTATGCCGGTTTCAGACAGGGACACGTTCTCCTTCGACATCAGCTTGCCCG
AGAAGATTCACTCTTATGAAAGAATGGAGTTTGCTGTGTACTACGAGTGCAATGGACAGACGTACTGGGA
CAGCAACAGAGGCAAGAATATAGGATCATCCGGGCTGAGTTAAAATCTACCCAGGGAATGACCAAGCCC
CACAGTGGACCGGATTTGGGAATATCCTTTGACCAGTTCGGAAGCCCTCGGTGTTCTTATGGTCTGTTTC
CAGAGTGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTAC**TAG**TGACTGCAGGTGACAGGGCG
TGGCGGAGCTGCCACA

FIG. 27

MMAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKKVKKRVSFADNQG
LALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADYLDFRNRLQADHVCLENCVL
KDKAIAAGTVKVQNLAFEKTVKIRMTFTWKSYSYTDFFCQYVKDTYAGSDRDTFSFDISLPEKIQSYERMEF
AVYYECNGQTYWDSNRGKNYRIIRAELKSTQGMTKPHSGPDLGISFDQFGSPRCSYGLFPEWPSYLGYEK
LGPYY

FIG. 28

Score = 3195 (479.4 bits), Expect = 2.8e-138, P = 2.8e-138
Identities = 763/903 (84%), Positives = 763/903 (84%), Strand = Plus / Plus

Query: 6 AGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAAC 65
AG TTCTAGCCTG C TCTA C TGATGGC GTGGACAT GA TACAG TACA C
Sbjct: 65 AGACTTCTAGCCTGCCCTCTAACG---TGATGGCCGTGGACATAGAATACAGCTACAGC 121

Query: 66 TGCATGGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACAAAGCCCAGC 125
G ATGC CCTTC TGC GC AGAG G TT CCTT AAGATCTC CC AA C A C
Sbjct: 122 AGTATGGCCCTTCTCTGCGCAGAGAGCGCTTCACCTTCAAGATCTCCCCAAACTGAAC 181

Query: 126 AAACCACTGAGGCCTTGTATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGGAAATGGTGGCC 185
AA CCAC TAGGCCTTGTATTTCAGCTG GCAGCAAG ATGAAGCC G GAATGGTGGCC
Sbjct: 182 AAGCCACTGAGGCCTTGTATTTCAGCTGGGCAGCAAGGATGAAGCCGGCAGAATGGTGGCC 241

Query: 186 CCGGCTGTCCAGGAGAAGAAGGTGAAAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTG 245
CC C GT CAGGAGAAGAAGGTGAA AAGCGGGTGTCTTCGC GACAACCAGGGGCTG
Sbjct: 242 CCCACAGTACAGGAGAAGAAGGTGAAGAAGCGGGTGTCTTCGCCGACAACCAGGGGCTG 301

Query: 246 GCCCTGACAATGGTCAAAGTGTCTCGGAATTCGATGACCCGCTAGATATGCCATTCAAC 305
GCCCT ACAATGGT AAAGTGTCTCGGAATTCGATGACCC CTAGATAT CC TT AAC
Sbjct: 302 GCCCTAACAAATGGTGAAGTGTCTCGGAATTCGATGACCCACTAGATATTCCGTTTAAAC 361

Query: 306 ATCACCAGAGCTCCTAGACAACATTTGTGAGCTTGACGACAGCAGAGAGCGAGAGCTTTGT 365
ATCAC GAGCTCCTAGACAACAT GTGAG TGACGACAGCAGAGAG GAGAGCTTTGT
Sbjct: 362 ATCACTGAGCTCCTAGACAACATCGTGAGTCTGACGACAGCAGAGAGTGAGAGCTTTGT 421

Query: 366 CTGGATTTTTCAGGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGGCCGAC 425
TGGATTTT C CAGCC TCTGCAGATTACTTAGACTTTAGAAATCG CTTCAG CC AC
Sbjct: 422 TTGGATTTTTCAGGCCCTCTGCAGATTACTTAGACTTTAGAAATCGGCTTCAGACCAAC 481

Query: 426 CACGTCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCACGTGAAGGTT 485
CA GTCTGCCT GA AACTG GTGCT AAGGA AA GCCAT GC GGCAC GT AAGGT
Sbjct: 482 CATGTCTGCCTCGAAAACATGCGTGCTGAAGGAGAAAGCCATCGCGGGCACCGTCAAGGTC 541

Query: 486 CAGAACCTCGCATTGAGAAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGC 545
CAGAACCT GCATT GAGAAG GTGAA AT AG ATGAC TTCGA ACCTGGAA AGC
Sbjct: 542 CAGAACCTGGCATTGAGAAAGGTTGTGAAGATCAGCATGACATTTCGATACCTGGAAGAGC 601

Query: 546 TACACAGACTTTCCTTGTGAGTACGTGAAGGACACTTATGCCGGTTTCAGACAGGGACACG 605
T CACAGACTT CCTTGTGAGTA GTGAAGGACACTTA GC GGTTCAGACAGGGACAC
Sbjct: 602 TTCACAGACTTCCCTTGTGAGTATGTGAAGGACACTTACGCTGGTTTCAGACAGGGACACA 661

Query: 606 TTCTCCTTCGACATCAGCTTGCCCCGAGAAGATTCACTCTTATGAAAGAATGGAGTTTGCT 665
TTCTCCTT GA ATCAGC T CC GAGAA AT CAGTCTTATGAAAGAATGGAGTT GC
Sbjct: 662 TTCTCCTTGTATATCAGCCTACCGGAGAAAATCCAGTCTTATGAAAGAATGGAGTTTCGCC 721

Query: 666 GTGTACTACGAGTGCAATGGACAGACGTAAGGACAGCAACAGAGGCAAGAATATAGG 725
GTGT CTACGAGTG AA GG CAG CGTACTGGGACAGCAACA AGGCAA AACTA AGG
Sbjct: 722 GTGTGCTACGAGTGTAACGGCCAGTCGTACTGGGACAGCAACAAAGGCAAAACTACAGG 781

Query: 726 ATCATCCGGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCCCACAGTGGACCGGAT 785
ATCA C GGGC GA T A ATC ACCCAGGGAATGAC AGCC ACA TGG CCGGAT
Sbjct: 782 ATCACCAGGGCCGAACCTCAGATCCACCCAGGGAATGACTGAGCCGTACAATGGGCCGGAT 841

Query: 786 TTGGGAATATCCTTTGACCAGTTTCGGAAGCCCTCGGTGTTCTCTATGGTCTGTTTCCAGAG 845
TT GGAAT TC TTTGACCAGTTTCGG AGCCCTCGGTGTTCTT GG CTGTTTCCAGAG
Sbjct: 842 TTTGGAATCTCTTTTGACCAGTTTCGGGAGCCCTCGGTGTTCTCTCGGCCGTGTTTCCAGAG 901

Query: 846 TGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGA-----CTGCAGG 900
TGGCC AGTTA T GG TATGAAAAGCT GGGCCCTA TACTAGTGA CTGCAG
Sbjct: 902 TGGCCTAGTTATCTGGGGTATGAAAAGCTGGGGCCCTATTACTAGTGAAGTTGACTGCACT 961

Query: 901 TGACAG 906
TGACAG
Sbjct: 962 TGACAG 967

FIG. 29

Score = 1366 (480.9 bits), Expect = 1.3e-139, P = 1.3e-139
Identities = 255/284 (89%), Positives = 270/284 (95%)

Query: 2 MAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKKVKK 61
MAVDIEY Y+ MAPSLR+ERF FKISPK +KPLRPCIQL SK+EA MVAP VQEKKVKK
Sbjct: 1 MAVDIEYSYSSMAPSLRRERFTFKISPKLNKPLRPCIQLGSKDEAGRMVAPTQVEKKVKK 60

Query: 62 RVSFADNQGLALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADY 121
RVSFADNQGLALTMVKVFSEFDDPLD+PFNITELLDNIVSLTTAESESFVLDF QPSADY
Sbjct: 61 RVSFADNQGLALTMVKVFSEFDDPLDIPFNITELLDNIVSLTTAESESFVLDFPQPSADY 120

Query: 122 LDFRNRLQADHVCLENCVLKDKAIAAGTVKVQNLAFEKTVKIRMTFDTWKS+TDFPCQYVK 181
LDFRNRLQ +HVCLENCVLK+KAIAGTVKVQNLAFEK VKIRMTFDTWKS+TDFPCQYVK
Sbjct: 121 LDFRNRLQTNHVCLENCVLKEKAIAGTVKVQNLAFEKVVKIRMTFDTWKSFTDFPCQYVK 180

Query: 182 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVYYECNGQTYWDSNRGKNYRIIRAELKSTQ 241
DTYAGSDRDTFSFDISLPEKIQSYERMEFAV YECNGQ+YWDSN+GKNYRI RAEL+STQ
Sbjct: 181 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVCYECNGQSYWDSNKGKNYRITRAELRSTQ 240

Query: 242 GMTKPHSGPDLGISFDQFGSPRCSYGLFPEWPSYLGYEKLGOPY 285
GMT+P++GPD GISFDQFGSPRCS+GLFPEWPSYLGYEKLGOPY
Sbjct: 241 GMTEPYNGPDLGISFDQFGSPRCSFGLFPEWPSYLGYEKLGOPY 284

FIG. 30

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

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Q63759_PP1_RAT      -----MAYDIEYSYSSMAPSLR--RERFTFKISPKLNKPLRPCIQLG
AC016485_A          -----MAYDIEYRYNCMAPSLR--QERFAFKISPKPSKPLRPCIQLS
O08541_PP1_MOUSE    -----MAMRICLAHSPPPLKSFLLGPNYNGFQRRNFVNKLKPLKPLCSV-
AAD33215_PPP1R5_HUMAN MIQVLDPRPLTSSVMPVDVAMRECLAHSPPVKSFLLGPNYDEFQRRHFVNKLKPLKSCSINI-

Q63759_PP1_RAT      SKDEAGRMVAPPTVQEKKVKKRVSFADNQGLALTMVKVFSEFDDP--LDIPFNITELLNDI
AC016485_A          SKDEAGSMVAPPAVQEKKVKKRVSFADNQGLALTMVKVFSEFDDP--LDMPFNITELLNDI
O08541_PP1_MOUSE    -KQEAKSQSEWKSPHNQAKKRVVFADSKGLSLTAIHVFSDLPEEPAWDLQFDLLDLNDIS
AAD33215_PPP1R5_HUMAN -KHKAKSQNDWKCSHNQAKKRVVFADSKGLSLTAIHVFSDLPEEPAWDLQFDLLDLNDIS

Q63759_PP1_RAT      VSLTTAESESFVLDFPQP SADYLDFRNRLQTNHVCLENCVLKPKAIACTVKVQNLAFEKV
AC016485_A          VSLTTAESESFVLDFSQPSADYLDFRNRLQADHVCLENCVLKDKAIACTVKVQNLAFEKT
O08541_PP1_MOUSE    SSLKLHEEKNLWFDFFQPSTDYLSFRDRFQKNFVCLENCSSLEDRVTCTVKVKNVSEFEKK
AAD33215_PPP1R5_HUMAN SALKHHEEKNLLDFDFPQPSTDYLSFRSHFQKNFVCLENCSSLEETVTCTVKVKNVSEFEKK

Q63759_PP1_RAT      VKIRMTFDTWKSFTDFPCQYVVKDTYAGSDRDTFSFDISLPEKIQSYERMEFAVCYECNGQ
AC016485_A          VKIRMTFDTWKSFTDFPCQYVVKDTYAGSDRDTFSFDISLPEKIQSYERMEFAVYECNGQ
O08541_PP1_MOUSE    VQVRITFDTWKTYTDVDCVYMKNVYSSSDSDTFSFAIDLPRVIPTEEKIEFCISYHANGR
AAD33215_PPP1R5_HUMAN VOIRITFDSWKNYTDVDCVYMKNVYGGTDSDTFSFAIDLPPVIPTEQKIEFCISYHANGQ

Q63759_PP1_RAT      SYWDSNKGKNYRITRAELR--STQGMTEFYN-----GPDFGISFDQFGSPRCSFGLFPE
AC016485_A          TYWDSNKGKNYRITRAELK--STQGMTKPHS-----GPDLGISFDQFGSPRCSYGLFPE
O08541_PP1_MOUSE    IFWDNNEGQNYRIVHVQWKPDGVQTQVAPKDCAFOGPPKTEIEPTVFGSPRLASGLFPE
AAD33215_PPP1R5_HUMAN VFWDNNDGQNYRIVHVQWKPDGVQTQMAPQDCARHOTSPTKELESTIFGSPRLASGLFPE

Q63759_PP1_RAT      WPSYLGYEKLGPIY
AC016485_A          WPSYLGYEKLGPIY
O08541_PP1_MOUSE    WQSWGRVENLTSYR
AAD33215_PPP1R5_HUMAN WQSWGRMENLASYR

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FIG. 31

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGC
TACTACCGCTTTGTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATC
AGCTTGGCTGTGCGGAAGATCGCGCTGCTGCTGAAGCCGGACAAGGAGATCGAACA
CCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTTCCGAAACTACACTGTGC
AGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGAAAA
TGCCAGATCTCATTCGTCGGTTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCC
CCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGG
CTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCCACCTCCACAAGGGC
TTCCTGGCCCTCTACCAAACCGTGGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGGC
TGGGGACTCAGGGACACCTGGGCTGGATCCCAGCCCTGCC

FIG. 32

MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFR
NYTVQFDVGVEFEEDLRSVDGRKCQISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSL
RLTFRTQPSSSENKTAHLHKGFLALYQTVALSGSLSDS

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

FIG. 33

Score = 355 (125.0 bits), Expect = 1.0e-31, P = 1.0e-31
Identities = 68/70 (97%), Positives = 70/70 (100%), Frame = +2

Query: 38 MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217
MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN
Sbjct: 1 MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query: 218 YTVQFDVGVE 247
YT+QFDVGV+
Sbjct: 61 YTLQFDVGVQ 70

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FIG. 34

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGCTACTACCGCTTT
GTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATCAGCTTGGCTGTGCGGAAGATCGCGC
TGCTGCTGAAGCCGGACAAGGAGATCGAACACCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTT
CCGAAACTACACTGTGCAGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGA
AAATGCCAGACCATAGTAACCTGGGAGGAGGAGCACCTGGTGTGTGTGCAGAAAGGGGAGGTCCTCCAACC
GGGGCTGGAGACACTGGCTGGAGGGAGAGTTGCTGTATCTGGAAGTGAAGGATGCAGTGTGCGA
GCAGGTCTTCAGGAAGGTCAGATAGCCGGAGAGGAGCCAAGATCCCTCCAGACAGCACCAGCTCACAGAC
GCTCTTGTGTGCCCCCTTCAAGCCCAGATTGTGCCAGATCTCATTTCGTCGGTTCGGATCCAAGCCAGTT
CTGTGGTCAGCAAGGCTCCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGT
TTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCACCTCCACAAGGGCTTCCTGG
CCCTCTACCAAACCGTGGGTGAGTGTCCCTCCTGGGGCTGCAGGGAGGGAGCCTCTGTTCCAGCCATGA
CCCTGGTATCTTCAAGCCTTAAGTGAAGCTTGAGTGACAGCTGAGG

FIG. 35

MPPNLTGYRFRVFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVGVE
FEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGELLYLELTARDAVCEQVFRKVR

1000 900 800 700 600 500 400 300 200 100 0

Score = 712 (250.6 bits), Expect = 1.5e-69, P = 1.5e-69
Identities = 133/135 (98%), Positives = 135/135 (100%), Frame = +2

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|--------|-----|--|-----|
| Query: | 38 | MPPNLTGYRFRVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN | 217 |
| | | MPPNLTGYRFRVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN | |
| Sbjct: | 1 | MPPNLTGYRFRVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN | 60 |
| | | | |
| Query: | 218 | YTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLCVCQKGEVPNRGWRHWLEGEMLYLEL | 397 |
| | | YT+QFDVGVEFEEDLRSVDGRKCQTIVTWEEHLCVCQKGEVPNRGWRHWLEGE+LYLEL | |
| Sbjct: | 61 | YTLQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLCVCQKGEVPNRGWRHWLEGEMLYLEL | 120 |
| | | | |
| Query: | 398 | TARDAVCEQVFRKVR | 442 |
| | | TARDAVCEQVFRKVR | |
| Sbjct: | 121 | TARDAVCEQVFRKVR | 135 |

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| Year | 1900 | 1901 | 1902 | 1903 | 1904 | 1905 | 1906 | 1907 | 1908 | 1909 | 1910 | 1911 | 1912 | 1913 | 1914 | 1915 | 1916 | 1917 | 1918 | 1919 | 1920 | 1921 | 1922 | 1923 | 1924 | 1925 | 1926 | 1927 | 1928 | 1929 | 1930 | 1931 | 1932 | 1933 | 1934 | 1935 | 1936 | 1937 | 1938 | 1939 | 1940 | 1941 | 1942 | 1943 | 1944 | 1945 | 1946 | 1947 | 1948 | 1949 | 1950 | 1951 | 1952 | 1953 | 1954 | 1955 | 1956 | 1957 | 1958 | 1959 | 1960 | 1961 | 1962 | 1963 | 1964 | 1965 | 1966 | 1967 | 1968 | 1969 | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| Population | 1,000,000 | 1,050,000 | 1,100,000 | 1,150,000 | 1,200,000 | 1,250,000 | 1,300,000 | 1,350,000 | 1,400,000 | 1,450,000 | 1,500,000 | 1,550,000 | 1,600,000 | 1,650,000 | 1,700,000 | 1,750,000 | 1,800,000 | 1,850,000 | 1,900,000 | 1,950,000 | 2,000,000 | 2,050,000 | 2,100,000 | 2,150,000 | 2,200,000 | 2,250,000 | 2,300,000 | 2,350,000 | 2,400,000 | 2,450,000 | 2,500,000 | 2,550,000 | 2,600,000 | 2,650,000 | 2,700,000 | 2,750,000 | 2,800,000 | 2,850,000 | 2,900,000 | 2,950,000 | 3,000,000 | 3,050,000 | 3,100,000 | 3,150,000 | 3,200,000 | 3,250,000 | 3,300,000 | 3,350,000 | 3,400,000 | 3,450,000 | 3,500,000 | 3,550,000 | 3,600,000 | 3,650,000 | 3,700,000 | 3,750,000 | 3,800,000 | 3,850,000 | 3,900,000 | 3,950,000 | 4,000,000 | 4,050,000 | 4,100,000 | 4,150,000 | 4,200,000 | 4,250,000 | 4,300,000 | 4,350,000 | 4,400,000 | 4,450,000 | 4,500,000 | 4,550,000 | 4,600,000 | 4,650,000 | 4,700,000 | 4,750,000 | 4,800,000 | 4,850,000 | 4,900,000 | 4,950,000 | 5,000,000 | 5,050,000 | 5,100,000 | 5,150,000 | 5,200,000 | 5,250,000 | 5,300,000 | 5,350,000 | 5,400,000 | 5,450,000 | 5,500,000 | 5,550,000 | 5,600,000 | 5,650,000 | 5,700,000 | 5,750,000 | 5,800,000 | 5,850,000 | 5,900,000 | 5,950,000 | 6,000,000 | 6,050,000 | 6,100,000 | 6,150,000 | 6,200,000 | 6,250,000 | 6,300,000 | 6,350,000 | 6,400,000 | 6,450,000 | 6,500,000 | 6,550,000 | 6,600,000 | 6,650,000 | 6,700,000 | 6,750,000 | 6,800,000 | 6,850,000 | 6,900,000 | 6,950,000 | 7,000,000 | 7,050,000 | 7,100,000 | 7,150,000 | 7,200,000 | 7,250,000 | 7,300,000 | 7,350,000 | 7,400,000 | 7,450,000 | 7,500,000 | 7,550,000 | 7,600,000 | 7,650,000 | 7,700,000 | 7,750,000 | 7,80 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |